Access DB# 52516

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name _____ Examiner # _____ Date: _____
Art Unit: _____ Phone Number 30_____ Serial Number _____
Mail Box and Bldg Room Location _____ Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

****

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: _____

Inventors (please provide full names): _____

_____

Earliest Priority Filing Date: _____

**For Sequence Searches Only* Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.*

Point of Contact:
Jan Delaval
Librarian
CM[illegible]

****

STAFF USE ONLY	Type of Search	Vendors and cost where applicable
Searcher: JAC	NA Sequence (#): _____	STN: _____
Searcher Phone #: 4498	AA Sequence (#): 2	Dialog: _____
Searcher Location: _____	Structure (#): _____	Questel/Orbit: _____
Date Searcher Picked Up: 10/9	Bibliographic: _____	Lexis/Nexis: _____
Date Completed: 10/9	Litigation: _____	Sequence Systems: ✓
Searcher Prep & Review Time: _____	Fulltext: _____	WWW/Internet: _____
Clerical Prep Time: 10	Patent Family: _____	Other (specify): _____
Online Time: 10	Other: _____	

PTO-1590 (8-2001)

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 14:13:15 ; Search time 1461.48 Seconds
(without alignments)
2519.074 Million cell updates/sec

Title: US-09-341-829A-4_COPY_756_993
Perfect score: 238
Sequence: 1 cagcttcccctgttgatgttg.....aaagctgagctacgattccg 238

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 1444157 seqs, 773887588 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2888314

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database : GenEmbl:*
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94: qb_ro1:*
95: qb_ro2:*
96: qb_in4:*
97: qb_pro:*
98: em_ba3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% query Match	Length	DB	ID	Description
1	238	100.0	1002	9	AK042585	AK042585 Sequence
2	238	100.0	1002	92	HSA223649	AL223649 Homo sapi
3	238	100.0	3245	91	HUS223093	AL223093 Homo sapi
c 4	238	100.0	112874	78	AF277315	AF277315 Homo sapi
5	233	97.9	679	9	AX024685	AX024685 Sequence
6	233	97.9	679	92	HSA012833	AL012833 Homo sapi
7	233	97.9	755	9	AK042536	AK042536 Sequence
8	233	97.9	755	92	HSA223041	AL223041 Homo sapi

	9	233	97.9	767	9	AX024687	AX024687 Sequence
	10	233	97.9	767	92	HSA012834	AJ012834 Homo sapi
	11	233	97.9	993	9	AX024689	AX024689 Sequence
	12	233	97.9	993	91	BC002833	BC002833 Homo sapi
	13	233	97.9	993	92	HSA012835	AJ012835 Homo sapi
	14	170	71.4	752	9	AR037873	AR037873 Sequence
	15	170	71.4	752	9	AX024691	AX024691 Sequence
	16	170	71.4	752	9	AX024693	AX024693 Sequence
	17	170	71.4	752	10	AX079857	AX079857 Sequence
	18	170	71.4	752	97	HSU87459	U87459 Human autoi
	19	170	71.4	755	9	AR042537	AR042537 Sequence
	20	170	71.4	755	92	HSA003149	AJ003149 Homo sapi
	21	170	71.4	806	88	AF038567	AF038567 Homo sapi
	22	170	71.4	873	93	HSA275978	AJ275978 Homo sapi
	23	170	71.4	2630	93	HSA275977	AJ275977 Homo sapi
	24	170	71.4	112874	78	AF277315	AF277315 Homo sapi
	25	24	10.1	217	9	AR042532	AR042532 Sequence
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c	27	20	8.4	22	9	AX024702	AX024702 Sequence
c	28	20	8.4	22	10	AX079859	AX079859 Sequence
	29	20	8.4	1042	53	CNS07CA9	AL438919 T3 end of
c	30	20	8.4	184144	76	AC079734	AC079734 Mus muscu
c	31	19	8.0	19	9	AR042534	AR042534 Sequence
c	32	19	8.0	19	9	AR042539	AR042539 Sequence
	33	19	8.0	1898	10	I46765	I46765 Sequence 1
c	34	19	8.0	2941	8	XLU85969	U85969 Xenopus lae
	35	19	8.0	118429	79	AL158017	AL158017 Homo sapi
	36	19	8.0	127178	87	AC010490	AC010490 Homo sapi
	37	19	8.0	154677	61	AC009901	AC009901 Homo sapi
	38	19	8.0	160771	92	HS88L2	AL035091 Human DNA
	39	19	8.0	165228	85	AC005325	AC005325 Homo sapi
	40	19	8.0	172051	71	AC044914	AC044914 Homo sapi
c	41	19	8.0	176092	74	AC073252	AC073252 Homo sapi
c	42	19	8.0	181144	90	AL365444	AL365444 Human DNA
	43	19	8.0	183196	76	AC083924	AC083924 Homo sapi
	44	19	8.0	184477	70	AC026277	AC026277 Homo sapi
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	46	19	8.0	187691	80	AL359982	AL359982 Homo sapi
	47	19	8.0	188775	70	AC026537	AC026537 Homo sapi
c	48	19	8.0	212390	80	AL356275	AL356275 Homo sapi
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c	50	18	7.6	3010	8	XLU85970	U85970 Xenopus lae

ALIGNMENTS

RESULT 1
AR042535
LOCUS AR042535 1002 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5811519.
ACCESSION AR042535
VERSION AR042535.1 GI:5963031
KEYWORDS .
SOURCE Unknown.
ORGANISM Unknown
Unclassified.
REFERENCE 1 (bases 1 to 1002)
AUTHORS Lethe ,B., Lucas,S., De Smet,C., Godelaine,D. and Boon-Falleur,T
TITLE LL-1 tumor specific genes
JOURNAL Patent: US 5811519-A 4 22-SEP-1998;
FEATURES Location/Qualifiers
source 1..1002
/organism="unknown"
BASE COUNT 179 a 302 c 336 g 185 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
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Qy 61 ccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatgcctcctccc 120
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Qy 121 [illegible] 180
Db 876 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCTGATTG[illegible] 935

Qy 181 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagctacgattccg 238
Db 936 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAGCTGAGCTACGATTCCG 993

RESULT 2
HSA223040
LOCUS HSA223040 1002 bp mRNA PRI 17-JUN-1998
DEFINITION Homo sapiens mRNA for LAGE-1b protein.
ACCESSION AJ223040
VERSION AJ223040.1 GI:3255992
KEYWORDS LAGE-1 gene.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1002)
AUTHORS Lethe,B.G.
TITLE Direct Submission
JOURNAL Submitted (06-JAN-1998) Lethe B.G., Brussels Branch, Ludwig
Institute for Cancer Research, 74, avenue Hippocrate, B-1200
Bruxelles, BELGIUM
REFERENCE 2 (bases 1 to 1002)
AUTHORS Lethe,B., Lucas,S., Michaux,L., De Smet,C., Godelaine,D.,
Serrano,A., De Plaen,E. and Boon,T.
TITLE LAGE-1, a new gene with tumor specificity
JOURNAL Int. J. Cancer 76 (6), 903-908 (1998)
MEDLINE 98289662
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/organism="Homo sapiens"
/isolate="individual LB373"
/db_xref="taxon:9606"
/chromosome="X"
/cell_line="LB373 MEL"
/cell_type="melanoma"
/map="q28"
/clone="LL-1.1"
/note="clone 2"
gene 65..976
/gene="LAGE-1"
CDS 65..697
/gene="LAGE-1"
/codon_start=1
/product="LAGE-1 protein"
/protein_id="CAA11043.1"
/db_xref="GI:3255993"
/translation="MQAEGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRG[illegible]
PRGAGAARASGPRGGAPRGPHGGAASAQ[illegible]
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polyA_signal 971..976
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polyA_site 993
BASE COUNT 179 a 302 c 336 g 185 t
ORIGIN

Query Match 100.0%; Score 238; DB 92; Length 1002;
Best Local Similarity 100.0%; Pred. No. 1e-130;
Matches 238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 ccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatgcctcctccc 120
Db        816 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCTTCCTAGGTCATGCCTCCTCCC 875

Qy        121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 180
Db        876 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCGCT 935

Qy        181 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagctacgattccg 238
Db        936 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAGCTGAGCTACGATTCCG 993


RESULT      3
HOS223093
LOCUS       HOS223093       3245 bp    DNA             PRI       23-JUN-1998
DEFINITION  Homo sapiens LAGE-1 gene.
ACCESSION   AJ223093
VERSION     AJ223093.1  GI:3255958
KEYWORDS    LAGE-1 gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 3245)
  AUTHORS   Lethe,B., Lucas,S., Michaux,L., De Smet,C., Godelaine,D.,
            Serrano,A., De Plaen,E. and Boon,T.
  TITLE     LAGE-1, a new gene with tumor specificity
  JOURNAL   Int. J. Cancer 76 (6), 903-908 (1998)
  MEDLINE   98289662
REFERENCE   2  (bases 1 to 3245)
  AUTHORS   Lethe,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (08-JAN-1998) Lethe B.G., Brussels Branch, Ludwig
            Institute for Cancer Research, 74 Avenue Hippocrate, B - 1200 -
            Bruxelles, BELGIUM
COMMENT     Related sequences: AJ223040, AJ223041 and AJ003149.
FEATURES             Location/Qualifiers
     source          1..3245
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                     /isolate="individual LB33"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /sex="Female"
                     /cell_line="LB33-MEL.A"
                     /cell_type="melanoma"
                     /map="q28"
                     /clone_lib="B6"
                     /clone="c2RB"
     gene            448..701
                     /gene="LAGE-1"
     repeat_region   448..701
                     /gene="LAGE-1"
                     /rpt_family="(ca)n repeat"
                     /rpt_unit=486..490
     misc_feature    766..1499
                     /gene="LAGE-1"
                     /note="CpG island"
     gene            766..2774
                     /gene="LAGE-1"
     GC_signal       1024..1029
                     /gene="LAGE-1"
     GC_signal       1145..1150
                     /gene="LAGE-1"
     mRNA            join(1167..1499,2115..2249,2479..2774)
                     /gene="LAGE-1"
     exon            1167..1499
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                     /number=1
     CDS             join(1231..1499,2115..2478)
                     /gene="LAGE-1"
                     /note="alternate splicing at exon 2 - intron 2 boundary"
                     /codon_start=1
                     /product="LAGE-1b protein"
                     /protein_id="CAA11117.1"
                     /db_xref="GI:3255960"
                     /db_xref="SPTREMBL:O75638"
                     /translation="MQAEGRGTGGSTGDADGP[illegible]
                     PRGAGAARASGPRGGAPRGPHGGAASAQDGRCPCGARRPDSRLLEGHLIMPESSEMEA
                     ELVRRILSRDAAPLPRPGAVLKDFTVSGNLLFM[illegible]
                     EGQKARDLRIPKRKVS[illegible]GVALNVMESAPHI"
     CDS             join(1231..1499,2115..2249,2479..2617)
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                     /codon_start=1
                     /product="LAGE-1a protein"
                     /protein_id="CAA11116.1"
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     variation       1247
                     /gene="LAGE-1"
                     /citation=[1]
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     exon            2115..2249
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     intron          2250..2478
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                     /citation=[1]
                     /replace="c"
     exon            2479..2774
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                     /number=3
     polyA_signal    2752..2757
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ORIGIN

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  Best Local Similarity   100.0%;  Pred. No. 1.1e-130;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 ccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatgcctcctccc 120
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Qy      121 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 180
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Db     2657 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCCTGATTGTTTGTCGCT 2716

Qy      181 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagctacgattccg 238
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     2717 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAGCTGAGCTACGATTCCG 2774


RESULT    4
AF277315/c
LOCUS       AF277315   112874 bp    DNA             HTG       05-NOV-2000
DEFINITION  Homo sapiens chromosome X clone RP5-865E18, RP5-1087L19 map q28,
            *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.
ACCESSION   AF277315
VERSION     AF277315.2  GI:11095455
KEYWORDS    HTG; HTGS_PHASE2.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 112874)
  AUTHORS   Galgoczy,P., Schilhabel,M., Rosenthal,A. and Platzer,M.
  TITLE     Chromosome X genomic sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 112874)
  AUTHORS   Galgoczy,P. and Platzer,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (13 JUN-2000) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenberstr. 11, Jena, Thuringia 07745, Germany
COMMENT     On Nov 5, 2000 this sequence version replaced gi:8705257.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1    94456: contig of 94456 bp in length
            *    94457    94556: gap of unknown length
            *    94557   112874: contig of 18318 bp in length.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="q28"
                     /clone="RP5-865E18, RP5-1087L19"
                     /clone_lib="RP5, RPCI human PAC library 5"
     misc_feature    1..30255
                     /note="overlap with Acc_number L44140"
     misc_feature    1..4
                     /note="RP5-865E18 clone end, SP6"
     misc_feature    4013..4016
                     /note="RP5-1087L19 clone end, SP6"
     gene            22962..45799
                     /gene="NEMO"
                     /note="NEMO, NFkappaB essential modulator (IKBKG)"
BASE COUNT     26633 a  28477 c  29739 g  27924 t    101 others
ORIGIN


  Query Match             100.0%;  Score 238;  DB 78;  Length 112874;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-130;
  Matches  238;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    99097 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGGCT [illegible]

Qy       61 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctccc 120
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Db    99037 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 98978

Qy      121 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 180
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Db    98977 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCCTGATTGTTTGTCGCT 98918

Qy      181 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagctacgattccg 238
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Db    98917 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAGCTGAGCTACGATTCCG 98860


RESULT    5
AX024685
LOCUS       AX024685       679 bp    DNA             PAT       1?-SEP-2000
DEFINITION  Sequence 1 from Patent EP1001022.
ACCESSION   AX024685
VERSION     AX024685.1  GI:10184771
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   Aarnoudse,C.A. and Schrier,P.
  TITLE     Camel, an alternative translation product of the tumour antigen
            lage-1
  JOURNAL   Patent: EP 1001022-A 1 17-MAY-2000;
            BOEHRINGER INGELHEIM INT (DE) , UNIV HOSPITAL LEIDEN (NL)
FEATURES             Location/Qualifiers
     source          1..679
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     5'UTR           1..9
     CDS             10..339
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC08996.1"
                     /db_xref="GI:10184772"
                     /translation="MLMAQEALAFLMAQGAMLAAQERRVPRAAEVPGAQGQQGPRGRE
                     EAPPGVRMAVPLLRRMEGAPAGPGGRTAACFSCTSRCLSRRPWKRSWSAGSCPGMPHL
                     SPDQGRP"
     3'UTR           340..679
BASE COUNT      120 a    208 c    221 g    130 t
ORIGIN


  Query Match             97.9%;  Score 233;  DB 9;  Length 679;
  Best Local Similarity   100.0%;  Pred. No. 9.4e-128;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      432 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGGCT 491

Qy       61 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctccc 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      492 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 551

Qy      121 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      552 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCCTGATTGTTTGTCGCT 611

Qy      181 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagctacga 233
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      612 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAGCTGAGCTACGA 664


RESULT    6
HSA012833
```

```
LOCUS       HSA012833     679 bp    mRNA            PRI       13-NOV-1999
DEFINITION  Homo sapiens mRNA for CTL-recognized antigen on melanoma (CAMEL).
ACCESSION   AJ012833
VERSION     AJ012833.1  GI:3893216
KEYWORDS    CAMEL gene; CTL-recognized antigen on melanoma (CAMEL).
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 679)
  AUTHORS   Aarnoudse,C.A., van den Doel,P.B., Heemskerk,B. and Schrier,P.I.
  TITLE     Interleukin-2-induced, melanoma-specific T cells recognize CAMEL,
            an unexpected translation product of LAGE-1
  JOURNAL   Int. J. Cancer 82 (3), 442-448 (1999)
  MEDLINE   99325550
REFERENCE   2  (bases 1 to 679)
  AUTHORS   Aarnoudse,C.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-NOV-1998) Aarnoudse C.A., Clinical Oncology, Leiden
            University Medical Center, P.O. Box, Leiden 2300 RC, The
            Netherlands
FEATURES             Location/Qualifiers
     source          1..679
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
                     /tissue_type="melanoma"
                     /cell_line="518/IL2.14"
                     /clone="4H8"
                     /note="5'truncated LAGE 1S cDNA clone"
     gene            10..339
                     /gene="CAMEL"
     CDS             10..339
                     /gene="CAMEL"
                     /codon_start=1
                     /product="CTL-recognized antigen on melanoma (CAMEL)"
                     /protein_id="CAA10193.1"
                     /db_xref="GI:3893217"
                     /db_xref="SPTREMBL:O95987"
                     /translation="MLMAQEALAFLMAQGAMLAAQERRVPRAAEVPGAQGQQGPRGRE
                     EAPRGVRMAVPLLRRMEGAPAGPGGRTAACFSCTSRCLSRRPWKRSWSAGSCPGMPHL
                     SPDQGRF"
BASE COUNT      120 a    208 c    221 g    130 t
ORIGIN

  Query Match             97.9%;  Score 233;  DB 92;  Length 679;
  Best Local Similarity   100.0%;  Pred. No. 9.4e-128;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGGCT 491

Qy         61 ccctcagggcagaggcgctaagcccagcctggcgcccccttcctaggtcatgcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 551

Qy        121 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcggct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCCTGATTGTTTGTCGGCT 611

Qy        181 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagctacga 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAGCTGAGCTACGA 664


RESULT    7
AR042536
LOCUS       AR042536      755 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 6 from patent US 5811519.
ACCESSION   AR042536
VERSION     AR042536.1  GI:5963032
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 755)
  AUTHORS   Lethe,B., Lucas,S., De Smet,C., Godelaine,D. and Boon-Falleur,T.
  TITLE     LL-1 tumor specific genes
  JOURNAL   Patent: US 5811519-A 6 22-SEP-1998;
FEATURES             Location/Qualifiers
     source          1..755
                     /organism="unknown"
BASE COUNT      126 a    234 c    252 g    143 t
ORIGIN

  Query Match             97.9%;  Score 233;  DB 9;  Length 755;
  Best Local Similarity   100.0%;  Pred. No. 9.4e-128;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGGCT 574

Qy         61 ccctcagggcagaggcgctaagcccagcctggcgcccccttcctaggtcatgcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 634

Qy        121 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcggct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCCTGATTGTTTGTCGGCT 694

Qy        181 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagctacga 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAGCTGAGCTACGA 747


RESULT    8
HSA223041
LOCUS       HSA223041     755 bp    mRNA            PRI       25-JUN-1998
DEFINITION  Homo sapiens mRNA for LAGE 1a protein.
ACCESSION   AJ223041
VERSION     AJ223041.1  GI:3255994
KEYWORDS    LAGE-1 gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 755)
  AUTHORS   Lethe,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-JAN-1998) Lethe B.G., Brussels Branch, Ludwig
            Institute for Cancer Research, 74, avenue Hippocrate, B-1200
            Bruxelles, BELGIUM
REFERENCE   2  (bases 1 to 755)
  AUTHORS   Lethe,B., Lucas,S., Michaux,L., De Smet,C., Godelaine,D.,
            Serrano,A., De Plaen,E. and Boon,T.
  TITLE     LAGE-1, a new gene with tumor specificity
  JOURNAL   Int. J. Cancer 76 (6), 903-908 (1998)
  MEDLINE   98289662
FEATURES             Location/Qualifiers
     source          1..755
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /cell_line="LB373 MEL"
                     /cell_type="Melanoma"
                     /map="q28"
                     /clone="LL-1.1"
                     /note="clone 4"
     gene            53..746
                     /gene="LAGE 1"
     CDS             53..595
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                     /gene="LAGE-1"
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                     /codon_start 1
                     /protein_id "CAA11044.1"
                     /db_xref="GI:3255995"
                     /translation "M[illegible]
                     PRGAGAARASCPRGCAPRGPHGGAASAQDGRCPCGARRPDSRLLQLHITMPFSSPMEA
                     ELVRRILSRDAAPLPRPGAVLKDFTV[illegible]
                     WITQCFLPVFLAQAPSGQRR"
     polyA_signal    730..735
                     /gene="LAGE-1"
     polyA_site      746
                     /gene="LAGE-1"
BASE COUNT      126 a    234 c    252 g    143 t
ORIGIN

  Query Match             97.9%;  Score 233;  DB 92;  Length 755;
  Best Local Similarity   100.0%;  Pred. No. 9.4e-128;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgttttggctcaggct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTGGCTCAGGCT 574

Qy         61 ccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatgcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCTTCCTAGGTCATGCCTCCTCCC 634

Qy        121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCGCT 694

Qy        181 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagctacga 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAGCTGAGCTACGA 747


RESULT 9
AX024687
LOCUS       AX024687      767 bp    DNA             PAT       15-SEP-2000
DEFINITION  Sequence 3 from Patent EP1001022.
ACCESSION   AX024687
VERSION     AX024687.1  GI:10184773
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 767)
  AUTHORS   Aarnoudse,C.A. and Schrier,P.
  TITLE     Camel, an alternative translation product of the tumour antigen
            lage-1
  JOURNAL   Patent: EP 1001022 A 2 17-MAY-2000;
            BOEHRINGER INGELHEIM INT (DE) ; UNIV HOSPITAL LEIDEN (NL)
FEATURES             Location/Qualifiers
     source          1..767
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
     5'UTR           1..53
     CDS             54..596
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id "CAC08947.1"
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                     /translation "MQAEG[illegible]
                     PRGAGAARASGPRGCAPRGPHGGAASAQDGRCPCGARRPDSRLLQLHITMPFSSPMEA
                     ELVRRILSRDAAPLPRPGAVLKDFTVSGNLLFIRLTAADHRQLQLSISSCLQQLSLLM
                     WITQCFLPVFLAQAPSGQRR"
     3'UTR           597..767
BASE COUNT      138 a    234 c    252 g    143 t
ORIGIN

  Query Match             97.9%;  Score 233;  DB 9;  Length 767;
  Best Local Similarity   100.0%;  Pred. No. 9.4e-128;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    ;  Gaps    ;

Qy          1 [illegible]
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Qy        121 [illegible]
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Db        636 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCGCT [illegible]

Qy        181 [illegible]
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 [illegible]


RESULT 10
HSA012834
LOCUS       HSA012834      767 bp    mRNA            PRI       [illegible]
DEFINITION  Homo sapiens mRNA for LAGE-1S and CTL-recognized antigen on
            melanoma (CAMEL).
ACCESSION   AJ012834
VERSION     AJ012834.1  GI:3893218
KEYWORDS    CAMEL gene; CTL recognized antigen on melanoma; LAGE-1S gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 767)
  AUTHORS   Aarnoudse,C.A., van den Doel,P.B., Heemskerk,B. and Schrier,P.I.
  TITLE     Interleukin-2-induced, melanoma-specific T cells recognize CAMEL,
            an unexpected translation product of LAGE-1
  JOURNAL   Int. J. Cancer 82 (3), 442-448 (1999)
  MEDLINE   99325550
REFERENCE   2  (bases 1 to 767)
  AUTHORS   Aarnoudse,C.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-NOV-1998) Aarnoudse C.A., Clinical Oncology, Leiden
            University Medical Center, P.O. Box, Leiden [illegible]
            Netherlands
FEATURES             Location/Qualifiers
     source          1..767
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /chromosome "X"
                     /map "Xq28"
                     /tissue_type "melanoma"
                     /cell_line "518/IL-2.14"
                     /clone "LAGE-1S"
     CDS             54..596
                     /note "short (spliced) form of tumor antigen LAGE-1"
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                     /product "LAGE-1S protein"
                     /protein_id "CAA10194.1"
                     /db_xref "GI:3893219"
                     /translation "MQAEG[illegible]
                     [illegible]
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                     WITQCFLPVFLAQAPSGQRR"
     gene            94..423
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     CDS             94..423
                     /gene "CAMEL"
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                     /codon_start 1
                     /product "CTL-recognized antigen on melanoma (CAMEL)"
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                     /protein_id "CAA[illegible].1"
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                     SPDQGRF"
BASE COUNT      138 a    234 c    252 g    143 t
ORIGIN

  Query Match            97.9%;  Score 233;  DB 92;  Length 767;
  Best Local Similarity  100.0%;  Pred. No. 9.4e-128;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        516 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGGCT 575

Qy         61 ccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatgcctcctccc 120
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Db        576 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCTTCCTAGGTCATGCCTCCTCCC 635

Qy        121 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 180
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Db        636 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCCTGATTGTTTGTCGCT 695

Qy        181 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagctacga 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        696 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAGCTGAGCTACGA 748


RESULT 11
AX024689
LOCUS       AX024689       993 bp    DNA             PAT       15-SEP-2000
DEFINITION  Sequence 5 from Patent EP1001022.
ACCESSION   AX024689
VERSION     AX024689.1  GI:10184775
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   Aarnoudse,C.A. and Schrier,P.
  TITLE     Camel, an alternative translation product of the tumour antigen
            lage 1
  JOURNAL   Patent: EP 1001022 A 5 17 MAY 2000;
            BOEHRINGER INGELHEIM INT (DE) ; UNIV HOSPITAL LEIDEN (NL)
FEATURES             Location/Qualifiers
     source          1..993
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     5'UTR           1..55
     CDS             56..688
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                     /codon_start 1
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                     /db_xref "GI:10184776"
                     /translation "MQAEGQGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRG
                     PRGAGAARASGPRGGAPRGPHGGAASA[illegible]CAPPG[illegible]RLLQLHITMPFSSPMEA
                     ELVRRILSRDAAPLPRPGAVLKDFTVSGNLLFMSVRDQDREGAGRMRVVGWGLGSASP
                     EGQFARS[illegible]VALNVMESAPHT"
     3'UTR           689..993
BASE COUNT      184 a    295 c    334 g    180 t
ORIGIN

  Query Match            97.9%;  Score 233;  DB 9;  Length 993;
  Best Local Similarity  100.0%;  Pred. No. 9.6e-128;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        747 CAGCTTTCCCTGTTGATGTGGATCACGCAG[illegible]

Qy         61 ccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatg[illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        807 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCTTCCTAGGTCATG[illegible]

Qy        121 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 1[illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        867 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGC[illegible]

Qy        181 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagctacga 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        927 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAGCTGAGCTACGA 979


RESULT 12
BC002833
LOCUS       BC002833       993 bp    mRNA            PRI       [illegible]-MAR-[illegible]
DEFINITION  Homo sapiens, cancer/testis antigen 2, clone MGC:3883, mRNA,
            complete cds.
ACCESSION   BC002833
VERSION     BC002833.1  GI:12803968
KEYWORDS    MGC.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (05-FEB-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD [illegible]
            USA
  REMARK    NIH-MGC [illegible] URL: http://mgc.nci.nih.gov
COMMENT     Contact: Robert Strausberg, Ph.D.
            Tel: (301) 496-1550
            Email: Robert_Strausberg@nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: National Institutes of Health Intramural
            Sequencing Center (NISC),
            Gaithersburg, Maryland;
            Web site: http://[illegible]
            Contact: nisc_mgc@nhgri.nih.gov
            Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
            Benjamin,B., Blakesley,R.W., Bouffard,G.G., [illegible]
            Dietrich,N.L., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R.,
            Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., [illegible]
            McDowell,J., Pearson,R., Snyder,L., Stantripop,S., Thomas,P.J.,
            [illegible] Walker,M.A.,
            Zhang,L.-H. and Green,E.D.

            Clone distribution: MGC clone distribution [illegible]
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FEATURES             Location/Qualifiers
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                     /clone "MGC:3883 IMAGE:[illegible]"
                     /tissue_type "Placenta, choriocarcinoma"
                     /clone_lib "NIH_MGC_21"
                     /lab_host "DH10B-R"
                     /note "Vector: pOTB7"
     CDS             28..660
                     /codon_start 1
                     /product "cancer/testis antigen 2"
                     /protein_id "AAH02833.1"
                     /db_xref "GI:12803969"
                     /translation "MQAEGRGTGGSTGDADG[illegible]
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                     PRGAGAARASGPRGGAPRGPHGGAASAQDGRCPCGARRPDSRLLQLHITMPFSSPMEA
                     ELVRRILSRDAAPLPRPGAVLKDFTVSGNLLFMSVRDQDREGAGRMRVVGWGLGSASP
                     EGQKARDLRTPKHKVSEQRPGTPGPPPPEGAQGDGCRGVAFNVMFSAPHI"
BASE COUNT      209 a    282 c    332 g    170 t
ORIGIN

  Query Match             97.9%;  Score 233;  DB 91;  Length 993;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-128;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgttttggctcagcct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      719 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTGGCTCAGCCT 778

Qy       61 ccctcagggcagaggcgctaagcccagcctggcgcccccttcctaggtcatgcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      779 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 838

Qy      121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttctcgct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      839 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTCTCGCT 898

Qy      181 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagctacga 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      899 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAGCTGAGCTACGA 951

RESULT 13
HSA012835
LOCUS       HSA012835     993 bp    mRNA            PRI       13-NOV-1999
DEFINITION  Homo sapiens mRNA for LAGE-1L and CTL-recognized antigen on
            melanoma (CAMEL).
ACCESSION   AJ012835
VERSION     AJ012835.1  GI:3893221
KEYWORDS    CAMEL gene; CTL-recognized antigen on melanoma (CAMEL); LAGE-1L
            gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 993)
  AUTHORS   Aarnoudse,C.A., van den Doel,P.B., Heemskerk,B. and Schrier,P.I.
  TITLE     Interleukin-2-induced, melanoma-specific T cells recognize CAMEL,
            an unexpected translation product of LAGE-1
  JOURNAL   Int. J. Cancer 82 (3), 442-448 (1999)
  MEDLINE   99325550
REFERENCE   2  (bases 1 to 993)
  AUTHORS   Aarnoudse,C.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (11-NOV-1998) Aarnoudse C.A., Clinical Oncology, Leiden
            University Medical Center, P.O. Box, Leiden 2300 RC, The
            Netherlands
FEATURES             Location/Qualifiers
     source          1..993
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="Xq28"
                     /tissue_type="melanoma"
                     /cell_line="518/IL2.14"
                     /clone="LAGE-1L"
     gene            56..688
                     /gene="LAGE-1L"
     CDS             56..688
                     /gene="LAGE-1L"
                     /note="long (unspliced) form of tumorantigen LAGE-1"
                     /codon_start=1
                     /product="LAGE-1L protein"
                     /protein_id="CAA10196.1"
                     /db_xref="GI:3893222"
                     /translation="MQAEGQGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRG
                     PRGAGAARASGPRGGAPRGPHGGAASAQDGRCPCGARRPDSRLLQLHITMPFSSPMEA
                     ELVRRILSRDAAPLPRPGAVLKDFTVSGNLLFMSVRDQDREGAGRMRVVGWGLGSASP
                     EGQKARDLRTPKHKVSEQRPGTPGPPPPEGAQGDGCRGVAFNVMFSAPHI"
     gene            96..425
                     /gene="CAMEL"
     CDS             96..425
                     /gene="CAMEL"
                     /note="alternative translation product of both LAGE-1S and
                     LAGE-1L"
                     /codon_start=1
                     /product="CTL-recognized antigen on melanoma (CAMEL)"
                     /protein_id="CAA10197.1"
                     /db_xref="GI:3893223"
                     /db_xref="SPTREMBL:O95987"
                     /translation="[illegible]
                     EAPRGVRMAVPLLRRMEGAPAGPGGRTAACFSCTSRCLSRRPWKRSWSAGSCPGMPHL
                     SPDQGRP"
BASE COUNT      184 a    295 c    334 g    180 t
ORIGIN

  Query Match             97.9%;  Score 233;  DB 92;  Length 993;
  Best Local Similarity   100.0%;  Pred. No. 9.6e-128;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgttttggctcagcct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      747 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTGGCTCAGCCT 806

Qy       61 ccctcagggcagaggcgctaagcccagcctggcgcccccttcctaggtcatgcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      807 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 866

Qy      121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttctcgct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      867 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTCTCGCT 926

Qy      181 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagctacga 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      927 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAAGCTGAGCTACGA 979

RESULT 14
AR037873
LOCUS       AR037873      752 bp    DNA             PAT       [illegible]
DEFINITION  Sequence 1 from patent US 5804381.
ACCESSION   AR037873
VERSION     AR037873.1  GI:5956590
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 752)
  AUTHORS   Chen,Y., Scanlan,M., Gure,A. and Old,L.J.
  TITLE     Isolated nucleic acid molecule encoding an esophageal cancer
            associated antigen, the antigen itself, and uses thereof
  JOURNAL   Patent: US 5804381-A 1 08-SEP-1998;
FEATURES             Location/Qualifiers
     source          1..752
                     /organism="unknown"
BASE COUNT      126 a    230 c    256 g    140 t
ORIGIN

  Query Match             71.4%;  Score 170;  DB 9;  Length 752;
  Best Local Similarity   99.5%;  Pred. No. 3.7e-90;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgttttggctcagcct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      516 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTGGCTCAGCCT 575

Qy       61 ccctcagggcagaggcgctaagcccagcctggcgcccccttcctaggtcatgcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db      576 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 635

Qy      121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      636 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCGCT 695

Qy      181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
            |||||||||||||||||||||||||||||||||||||||||
Db      696 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 736


RESULT 15
AX024691
LOCUS       AX024691       752 bp    DNA             PAT       15-SEP-2000
DEFINITION  Sequence 7 from Patent EP1001022.
ACCESSION   AX024691
VERSION     AX024691.1  GI:10184777
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 752)
  AUTHORS   Aarnoudse,C.A. and Schrier,P.
  TITLE     Camel, an alternative translation product of the tumour antigen
            Lage-1
  JOURNAL   Patent: EP 1001022-A 7 17-MAY-2000;
            BOEHRINGER INGELHEIM INT (DE) ; UNIV HOSPITAL LEIDEN (NL)
FEATURES             Location/Qualifiers
     source          1..752
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     5'UTR           1..53
     CDS             54..596
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC08999.1"
                     /db_xref="GI:10184778"
                     /translation="MQAEGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRG
                     PRGAGAARASGPGGGAPRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEA
                     ELARRSLAQDAPPLPVPGVLLKEFTVSGNILTIRLTAADHRQLQLSISSCLQQLSLLM
                     WITQCFLPVFLAQPPSGQRR"
     3'UTR           597..752
BASE COUNT      126 a    230 c    256 g    140 t
ORIGIN

  Query Match             71.4%;  Score 170;  DB 9;  Length 752;
  Best Local Similarity   99.5%;  Pred. No. 3.7e-90;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db      516 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGGCT 575

Qy       61 ccctcagggcagaggcgctaagcccagcctggcgcccctteetaggtcatgcctcctccc 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db      576 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 635

Qy      121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      636 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCGCT 695

Qy      181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
            |||||||||||||||||||||||||||||||||||||||||
Db      696 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 736


RESULT 16
AX024693
LOCUS       AX024693       752 bp    DNA             PAT       15-SEP-2000
DEFINITION  Sequence 9 from Patent EP1001022.
ACCESSION   AX024693
VERSION     AX024693.1  GI:10184779
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 752)
  AUTHORS   Aarnoudse,C.A. and Schrier,P.
  TITLE     Camel, an alternative translation product of the tumour antigen
            Lage-1
  JOURNAL   Patent: EP 1001022-A 9 17-MAY-2000;
            BOEHRINGER INGELHEIM INT (DE) ; UNIV HOSPITAL LEIDEN (NL)
FEATURES             Location/Qualifiers
     source          1..752
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     5'UTR           1..93
     CDS             94..270
                     /note="unnamed protein product"
                     /codon_start=1
                     /protein_id="CAC09000.1"
                     /db_xref="GI:10184780"
                     /translation="MLMAQEALAFLMAQGAMLAAQ...
                     EAPRGVRMAARLQG"
     3'UTR           271..752
BASE COUNT      126 a    230 c    256 g    140 t
ORIGIN

  Query Match             71.4%;  Score 170;  DB 9;  Length 752;
  Best Local Similarity   99.5%;  Pred. No. 3.7e-90;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db      516 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGGCT 575

Qy       61 ccctcagggcagaggcgctaagcccagcctggcgcccctteetaggtcatgcctcctccc 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||
Db      576 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 635

Qy      121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      636 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCGCT 695

Qy      181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
            |||||||||||||||||||||||||||||||||||||||||
Db      696 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 736


RESULT 17
AX079857
LOCUS       AX079857       752 bp    DNA             PAT       22-FEB-2001
DEFINITION  Sequence 1 from Patent WO0107917.
ACCESSION   AX079857
VERSION     AX079857.1  GI:13159992
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 752)
  AUTHORS   Jager,E., Stockert,E., Old,L.J., Knuth,A., Chen,Y.T. and ...
  TITLE     Determining antibodies to ny-eso-1 in cancer patients
  JOURNAL   Patent: WO 0107917-A 1 01-FEB-2001;
            LUDWIG INSTITUTE FOR CANCER RESEARCH (US) ; MEMORIAL
            SLOAN KETTERING CANCER CENTER (US) ; Cornell Research Foundat...
            (US)
FEATURES             Location/Qualifiers
     source          1..752
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
BASE COUNT      126 a    230 c    256 g    140 t
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ORIGIN

  Query Match             71.4%;  Score 170;  DB 10;  Length 752;
  Best Local Similarity   99.5%;  Pred. No. 3.7e-90;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcagcct 60
             |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db     516 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGCCT 575

Qy      61 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctcc 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 635

Qy     121 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCCTGATTGTTTGTCGCT 695

Qy     181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
             |||||||||||||||||||||||||||||||||||||||||
Db     696 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 736


RESULT 18
HSU87459
LOCUS       HSU87459      752 bp    mRNA            PRI       22-DEC-1999
DEFINITION  Human autoimmunogenic cancer/testis antigen NY-ESO-1 mRNA, complete
            cds.
ACCESSION   U87459
VERSION     U87459.1  GI:1890098
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 752)
  AUTHORS   Chen,Y.T., Scanlan,M.J., Sahin,U., Tureci,O., Gure,A.O., Tsang,S.,
            Williamson,B., Stockert,E., Pfreundschuh,M. and Old,L.J.
  TITLE     A testicular antigen aberrantly expressed in human cancers detected
            by autologous antibody screening
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 94 (5), 1914-1918 (1997)
  MEDLINE   97203161
   PUBMED   9050879
REFERENCE   2  (bases 1 to 752)
  AUTHORS   Chen,Y.-T.
  TITLE     Direct Submission
  JOURNAL   Submitted (28-JAN-1997) Ludwig Institute for Cancer Research, New
            York Branch, 1275 York Avenue, New York, NY 10021, USA
FEATURES             Location/Qualifiers
     source          1..752
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone_lib="esophageal squamous cell carcinoma expression
                     cDNA library"
     CDS             54..596
                     /codon_start=1
                     /product="autoimmunogenic cancer/testis antigen NY-ESO-1"
                     /protein_id="AAB49693.1"
                     /db_xref="GI:1890099"
                     /translation="MQAEGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRG
                     PRGAGAARASGPGGGAPRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEA
                     ELARRSLAQDAPPLPVPGVLLKEFTVSGNILTIRLTAADHRQLQLSISSCLQQLSLLM
                     WITQCFLPVFLAQPPSGQRR"
BASE COUNT      126 a    230 c    256 g    140 t
ORIGIN

  Query Match             71.4%;  Score 170;  DB 97;  Length 752;
  Best Local Similarity   99.5%;  Pred. No. 3.7e-90;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcagcct 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db     516 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGCCT 575

Qy      61 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctcc 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 635

Qy     121 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCCTGATTGTTTGTCGCT 695

Qy     181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
             |||||||||||||||||||||||||||||||||||||||||
Db     696 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 736


RESULT 19
AR042537
LOCUS       AR042537      755 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 9 from patent US 5811519.
ACCESSION   AR042537
VERSION     AR042537.1  GI:5963033
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 755)
  AUTHORS   Lethe,B., Lucas,S., De Smet,C., Godelaine,D. and Boon-Falleur,T.
  TITLE     LL-1 tumor specific genes
  JOURNAL   Patent: US 5811519-A 8 22-SEP-1998;
FEATURES             Location/Qualifiers
     source          1..755
                     /organism="unknown"
BASE COUNT      131 a    229 c    256 g    139 t
ORIGIN

  Query Match             71.4%;  Score 170;  DB 9;  Length 755;
  Best Local Similarity   99.5%;  Pred. No. 3.7e-90;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcagcct 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db     513 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGCCT 572

Qy      61 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctcc 120
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     573 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 632

Qy     121 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 180
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     633 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCCTGATTGTTTGTCGCT 692

Qy     181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
             |||||||||||||||||||||||||||||||||||||||||
Db     693 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 733


RESULT 20
HSA003149
LOCUS       HSA003149     755 bp    mRNA            PRI       27-JUN-1998
DEFINITION  Homo sapiens mRNA for NY-ESO-1 protein.
ACCESSION   AJ003149
VERSION     AJ003149.1  GI:3255960
KEYWORDS    NY-ESO-1 gene.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 755)
  AUTHORS   Lethe,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (02-JAN-1998) Lethe B.G., Brussels Branch, Ludwig
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            Institute for Cancer Research, 74, Avenue Hippocrate, B 1200
            Brussels, BELGIUM
REFERENCE   2  (bases 1 to 755)
  AUTHORS   Lethe,B., Lucas,S., Michaux,L., De Smet,C., Godelaine,D.,
            Serrano,A., De Plaen,E. and Boon,T.
  TITLE     LAGE-1, a new gene with tumor specificity
  JOURNAL   Int. J. Cancer 76 (6), 903-908 (1998)
  MEDLINE   98289662
FEATURES             Location/Qualifiers
     source          1..755
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /cell_line="LB373 MEL"
                     /cell_type="melanoma"
                     /map="q"
                     /clone="LL 1.2"
                     /clone_lib="pcDNA1/Amp"
                     /note="clone 3"
     gene            51..593
                     /gene="NY-ESO-1"
     CDS             51..593
                     /gene="NY-ESO-1"
                     /codon_start=1
                     /product="NY-ESO-1 protein"
                     /protein_id="CAA05908.1"
                     /db_xref="GI:3255991"
                     /db_xref="SWISS-PROT:P78358"
                     /translation="MQAEGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRG
                     PRGAGAARASGPGGGAPRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEA
                     ELARRSLAQDAPPLPVPGVLLKEFTVSGNILTIRLTAADHRQLQLSISSCLQQLSLLM
                     WITQCFLPVFLAQPPSGQRR"
BASE COUNT      131 a    229 c    256 g    139 t
ORIGIN

  Query Match             71.4%;  Score 170;  DB 92;  Length 755;
  Best Local Similarity   99.5%;  Pred. No. 3.7e-90;
  Matches  228;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 cagctttcctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        513 CAGCTTTCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGCCT 572

Qy         61 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctcc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCC 632

Qy        121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        633 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCGCT 692

Qy        181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
              |||||||||||||||||||||||||||||||||||||||||
Db        693 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 733


RESULT 21
AF038567
LOCUS       AF038567      806 bp    mRNA            PRI       16-JAN-1999
DEFINITION  Homo sapiens cancer antigen 3 and cancer antigen-3-ORF2 mRNA,
            complete cds.
ACCESSION   AF038567
VERSION     AF038567.1  GI:4164676
KEYWORDS    .
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 806)
  AUTHORS   Wang,R.-F., Johnston,S.L., Zeng,G., Topalian,S.L.,
            Schwartzentruber,D.J. and Rosenberg,S.A.
  TITLE     A Breast and Melanoma Shared Tumor Antigen: T Cell Responses to
            Antigenic Peptides Translated from Different Open Reading Frames
  JOURNAL   J. Immunol. 161, 3596-3606 (1998)
REFERENCE   2  (bases 1 to 806)
  AUTHORS   Wang,R.-F. and Rosenberg,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-DEC-1997) Surgery Branch, National Cancer Institute,
            9000 Rockville Pike, Bethesda, MD 20892, USA
FEATURES             Location/Qualifiers
     source          1..806
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
     CDS             89..631
                     /note="CAG-3; tumor antigen recognized by cytotoxic T
                     lymphocytes"
                     /codon_start=1
                     /product="cancer antigen 3"
                     /protein_id="AAD05202.1"
                     /db_xref="GI:4104677"
                     /translation="MQAEGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEAGATGGRG
                     PRGAGAARASGPGGGAPRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEA
                     ELARRSLAQDAPPLPVPGVLLKEFTVSGNILTIRLTAADHRQLQLSISSCLQQLSLLM
                     WITQCFLPVFLAQPPSGQRR"
     CDS             129..305
                     /note="CAG-3-ORF2"
                     /codon_start=1
                     /product="cancer antigen 3-ORF2"
                     /protein_id="AAD05203.1"
                     /db_xref="GI:4159898"
                     /translation="MLMAQEALAFLMAQGAMLAAQERRVPRAAEVPGAPGQGPRPRE
                     EAPRGVRMAARLQG"
BASE COUNT      155 a    236 c    270 g    145 t
ORIGIN

  Query Match             71.4%;  Score 170;  DB 88;  Length 806;
  Best Local Similarity   99.5%;  Pred. No. 3.8e-90;
  Matches  228;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 cagctttcctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        551 CAGCTTTCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGCCT 610

Qy         61 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctcc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        611 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCC 670

Qy        121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCGCT 730

Qy        181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
              |||||||||||||||||||||||||||||||||||||||||
Db        731 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 771


RESULT 22
HSA275978
LOCUS       HSA275978      873 bp    mRNA            PRI       09-MAR-2000
DEFINITION  Homo sapiens partial mRNA LAGE-2b for hypothetical protein (LAGE-2
            gene).
ACCESSION   AJ275978
VERSION     AJ275978.1  GI:7208842
KEYWORDS    LAGE-2 gene; LAGE-2b.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 873)
  AUTHORS   Lethe,B.G.
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 873)
  AUTHORS   Lethe,B.G.
  TITLE     Direct Submission
```

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  JOURNAL   Submitted (04 MAR 2000) Lethe B.G., Molecular Biology, Ludwig
            Institute for Cancer Research, 74, avenue Hippocrate, 1200 -
            Bruxelles, BELGIUM
FEATURES             Location/Qualifiers
     source          1..973
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /cell_line="Thyroid carcinoma cell line ATCC CRL1803"
     gene            1..844
                     /gene="LAGE-2"
     CDS             <1..429
                     /gene="LAGE-2"
                     /note="rare transcript LAGE-2b with retained intron 2
                     (327-565)"
                     /codon_start=1
                     /product="hypothetical protein"
                     /protein_id="CAB76945.1"
                     /db_xref="GI:7208843"
                     /translation="[illegible]
                     GLNGCCRCGARGPESRLLEFYLAMPFATPMEAELARRSLAQDAPPLPVPGVLLKEFTV
                     SGNILTMSVQDQDKDGAWVGGHSVAGWGLGSAYTPRSGC"
     polyA_signal    839..844
                     /gene="LAGE-2"
BASE COUNT      167 a    259 c    290 g    157 t
ORIGIN


  Query Match             71.4%;  Score 170;  DB 93;  Length 973;
  Best Local Similarity   99.5%;  Pred. No. 3.8e-90;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cagctttccctqttgatgtqgatcacqgcagtgcttttctgcccgtgttttgggctcagccc 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     624 CAGCTTTCCCTGTTGATGTGGATCACGGCAGTGCTTTCTGCCCGTGTTTTGGGCTCAGCCC 683

Qy      61 [illegible] 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     684 CCCTCAGGGCAGAGGGCTAAGCCCAGCCTGGCGGCCCTTCCTACGTCATGCCTCCTCCTCC 743

Qy     121 ctaqqaatqqtcccaqccacqaqtqqccaqttcattqtqqqqqcctgattgtttgtctqct 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     744 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCCTGATTGTTTGTCTGCT 803

Qy     181 quaqqaqqaccqqcttacatqttqtttctqtaqaaaataaa 221
           |||||||||||||||||||:||||||||||||||||||||
Db     804 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 844


RESULT 23
HSA275977
LOCUS       HSA275977    2630 bp    DNA             PRI       08 MAR 2000
DEFINITION  Homo sapiens LAGE 2 gene for NY ESO 1/LAGE 2a protein and
            alternative polypeptide LAGE 2alt, exons 1 *.
ACCESSION   AJ275977
VERSION     AJ275977.1  GI:7208839
KEYWORDS    CTL-defined antigenic peptide; LAGE 2 gene; LAGE 2a; LAGE 2alt.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2630)
  AUTHORS   De Smet,C., Lurquin,C., Lethe,B., Martelange,V. and Boon,T.
  TITLE     DNA methylation is the primary silencing mechanism for a set of
            germ line- and tumor-specific genes with a CpG-rich promoter
  JOURNAL   Mol. Cell. Biol. 19 (11), 7327-7335 (1999)
  MEDLINE   99454985
REFERENCE   2  (bases 1 to 2630)
  AUTHORS   Lethe,B.G.
  TITLE     Direct Submission
  JOURNAL   Submitted (04 MAR 2000) Lethe B.G., Molecular Biology, Ludwig
            Institute for Cancer Research, 74, avenue Hippocrate, 1200 -
            Bruxelles, BELGIUM
COMMENT     Related sequence AJ275978.rare LAGE 2 mRNA species retaining intron
            2 (LAGE-2b).
FEATURES             Location/Qualifiers
     source          1..2630
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /sex="M"
                     /note="gene isolated from human testis library, Bo 5 5"
     promoter        <1..907
                     /note="CpG island"
     mRNA            join(908..1240,1913..2047,2287..2577)
                     /gene="LAGE-2"
                     /note="LAGE-2a form"
     exon            908..1240
                     /gene="LAGE-2"
                     /number=1
     gene            908..2577
                     /gene="LAGE-2"
     CDS             join(972..1240,1913..2047,2287..2425)
                     /gene="LAGE-2"
                     /note="CTL defined antigenic peptides are processed from
                     this product"
                     /codon_start=1
                     /product="NY-ESO-1/LAGE-2a protein"
                     /protein_id="CAB76943.1"
                     /db_xref="GI:7208840"
                     /translation="MQAEGRGTGGSTGDADGPGGPGIPDGPGGNAGGPGEA[illegible]
                     PRGAGAARASGPGGGAPRGPHGGAASGLNGCCRCGARGPESRLLEFYLAMPFATPMEA
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                     WITQCFLPVFLAQPPSGQRR"
     CDS             1012..1188
                     /gene="LAGE-2"
                     /codon_start=1
                     /product="alternative polypeptide LAGE 2alt"
                     /protein_id="CAB76944.1"
                     /db_xref="GI:7208841"
                     /translation="MLMAQEALAFLMAQLAMLAAREAPRGVRMAARLQG"
     intron          1241..1912
                     /gene="LAGE-2"
                     /note="purine-rich (71.7%) with guanidine accounting for
                     53.9% of the total"
                     /number=1
     exon            1913..2047
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                     /number=2
     intron          2048..2286
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                     /number=2
     exon            2287..2577
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     polyA_signal    2560..2565
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     polyA_site      2577
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ORIGIN


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  Best Local Similarity   99.5%;  Pred. No. 4.1e-96;
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Qy      61 [illegible] 120
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Db    2405 CCCTCAGGGCAGAGGGCTAAGCCCAGCCTGGCGGCCCTTCCTACGTCATGCCTCCTCCTCC 2464

Qy     121 ctaqqaatqqtcccaqccacqaqtqqccaqttcattqtqqqqqcctgattgtttgtctqct 180
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Db    2465 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCGCT 2524

Qy     181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
           |||||||||||||||:|||||||||||||||||||||||||
Db    2525 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 2565


RESULT  24
AF277315
LOCUS       AF277315    112874 bp    DNA             HTG       05-NOV-2000
DEFINITION  Homo sapiens chromosome X clone RP5-865E18, RP5-1087L19 map q28,
            *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.
ACCESSION   AF277315
VERSION     AF277315.2  GI:11095455
KEYWORDS    HTG; HTGS_PHASE2.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 112874)
  AUTHORS   Galgoczy,P., Schilhabel,M., Rosenthal,A. and Platzer,M.
  TITLE     Chromosome X genomic sequence
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 112874)
  AUTHORS   Galgoczy,P. and Platzer,M.
  TITLE     Direct Submission
  JOURNAL   Submitted (13-JUN-2000) Genome Analysis, Institute of Molecular
            Biotechnology, Beutenbergstr. 11, Jena, Thuringia 07745, Germany
COMMENT     On Nov 5, 2000 this sequence version replaced gi:8705257.
            * NOTE: This is a 'working draft' sequence. It currently
            * consists of 2 contigs. Gaps between the contigs
            * are represented as runs of N. The order of the pieces
            * is believed to be correct as given, however the sizes
            * of the gaps between them are based on estimates that have
            * provided by the submittor.
            * This sequence will be replaced
            * by the finished sequence as soon as it is available and
            * the accession number will be preserved.
            *        1    94456: contig of 94456 bp in length
            *    94457    94556: gap of unknown length
            *    94557   112874: contig of 18318 bp in length.
FEATURES             Location/Qualifiers
     source          1..112874
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /chromosome="X"
                     /map="q28"
                     /clone="RP5-865E18, RP5-1087L19"
                     /clone_lib="RP5, RPCI human PAC library 5"
     misc_feature    1..40255
                     /note="overlap with Acc_number L44140"
     misc_feature    1..4
                     /note="RP5-865E18 clone end, SP6"
     misc_feature    4013..4016
                     /note="RP5-1087L19 clone end, SP6"
     gene            22962..45799
                     /gene="NEMO"
                     /note="NEMO, NFkappaB essential modulator (IKBKG)"
BASE COUNT    26633 a  28477 c  29739 g  27924 t    101 others
ORIGIN


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  Best Local Similarity   99.5%;  Pred. No. 5.1e-90;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
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Qy      61 ccctcagggcagaggcgctaagcccagcctggcgcccctteetaggtcatgcctcctccc 120
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Db   67411 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 67470

Qy     121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 180
           ||||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||
Db   67471 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCGCT 67530

Qy     181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
           |||||||||||||||:|||||||||||||||||||||||||
Db   67531 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 67571


RESULT  25
AR042532
LOCUS       AR042532      217 bp    DNA             PAT       29-SEP-1999
DEFINITION  Sequence 1 from patent US 5811519.
ACCESSION   AR042532
VERSION     AR042532.1  GI:5963028
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 217)
  AUTHORS   Lethe,B., Lucas,S., De Smet,C., Godelaine,D. and Boon-Falleur,T.
  TITLE     LL-1 tumor specific genes
  JOURNAL   Patent: US 5811519-A 1 22-SEP-1998;
FEATURES             Location/Qualifiers
     source          1..217
                     /organism="unknown"
BASE COUNT       48 a     72 c     53 g     44 t
ORIGIN


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  Best Local Similarity   100.0%;  Pred. No. 0.0047;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 cagctttccctgttgatgtggatc 24
           ||||||||||||||||||||||||
Db     194 CAGCTTTCCCTGTTGATGTGGATC 217


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Job time: 4920 sec
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Run on: October 9, 2001, 14:51:10 ; Search time 112.99 Seconds
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Searched: 730101 seqs, 313950809 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1466202

Minimum DB seq length: 0
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Post-processing: Listing first 50 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	238	100.0	1002	19	AAV50346	Human LAGE-1 clone
	2	233	97.9	679	21	AAD00149	Human CTL-recognis
	3	233	97.9	755	19	AAV50347	Human LAGE-1 clone
	4	233	97.9	767	21	AAD00150	Human LAGE-1 splic
	5	233	97.9	993	21	AAD00151	Human LAGE-1 unspl
	6	170	71.4	752	19	AAV38566	DNA encoding a can
	7	170	71.4	752	21	AAA61483	cDNA encoding huma
	8	170	71.4	752	21	AAD00152	Human tumour antig
	9	170	71.4	752	21	AAZ38380	Human tumour antig
	10	170	71.4	752	22	AAF58634	Human NY-ESO-1 nuc
	11	170	71.4	755	19	AAV50348	Human NY-ESO-1 nuc
	12	170	71.4	806	20	AAX58599	Human cancer antig
	13	24	10.1	217	19	AAV50349	Human LAGE-1 clone
c	14	22	9.2	22	20	AAX58604	Human cancer antig
c	15	21	8.8	21	21	AAD00156	Reverse PCR primer
c	16	20	8.4	32	19	AAV38568	PCR primer used t
c	17	20	8.4	32	21	AAD00159	LAGE-1 specific PC
c	18	20	8.4	32	21	AAZ49179	PCR primer for NY
c	19	20	8.4	32	21	AAZ38382	Human tumour antig
c	20	20	8.4	32	22	AAF58636	Human NY-ESO-1 PCR
c	21	19	8.0	19	19	AAV50351	Human LAGE-1 PCR p
c	22	19	8.0	19	19	AAV50353	Human LAGE-1 PCR p
	23	19	8.0	1898	18	AAT79634	DNA encoding human
c	24	18	7.6	1444	21	AAC53380	Arabidopsis thalia
c	25	18	7.6	2168	20	AAX99631	Genomic DNA sequen
c	26	17	7.1	32	20	AAX78866	Human tissue facto
c	27	17	7.1	533	21	AAC01342	Human secreted pro
	28	17	7.1	631	21	AAC33197	Arabidopsis thalia
c	29	17	7.1	1316	18	AAT63621	Interleukin 12 p35
c	30	17	7.1	1349	21	AAA38940	Staphylococcus aur
c	31	17	7.1	1364	17	AAT48099	Human interleukin
c	32	17	7.1	1364	19	AAV42536	Human interleukin
c	33	17	7.1	1364	19	AAV15228	Heterodimeric huma
c	34	17	7.1	1364	21	AAZ28863	Human interleukin
c	35	17	7.1	1364	22	AAF56281	IL-12 vaccine ant
c	36	17	7.1	1396	13	AAQ24371	Natural killer cel
c	37	17	7.1	1482	19	AAV27058	Aspergillus oryzae
	38	17	7.1	1622	21	AAC98948	Human pancreatic
	39	17	7.1	1688	17	AAT27617	Steroid hormone re
	40	17	7.1	1761	21	AAC42791	Arabidopsis thalia
	41	17	7.1	1813	16	AAQ88760	Human ubiquitous n
	42	17	7.1	1979	17	AAT27616	Human foetal kidn
	43	17	7.1	[illegible]	[illegible]	[illegible]	Human recombinant
	44	17	7.1	2030	17	AAT18996	Human steroid rec
	45	17	7.1	[illegible]	17	[illegible]	New receptor prote
	46	17	7.1	[illegible]	21	[illegible]	Arabidopsis thalia
	47	17	7.1	[illegible]	21	[illegible]	Arabidopsis thalia
	48	17	7.1	2683	21	[illegible]	Arabidopsis thalia
c	49	17	7.1	2987	20	AAZ25739	Aspergillus oryzae
[illegible]	50	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]	Aspergillus oryzae

ALIGNMENTS

RESULT 1
AAV50346
ID AAV50346 standard; cDNA; 1002 BP.
XX
AC AAV50346;
XX
DT [illegible]
XX
DE Human LAGE-1 clone 2 nucleotide sequence.
XX
KW Human; LAGE 1; tumour associated protein; LL 1; diagnosis; tumour; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 65..697
FT /*tag= a
FT /product= "LAGE 1"
XX
PN WO9832855-A1.
XX
PD 30-JUL-1998.
XX
PF 27-JAN-1998; 98WO-US01445.
XX
PR 27-JAN-1997; 97US-0791495.
XX
PA (LUDW) LUDWIG INST CANCER RES.
XX

PI Boon-Falleur T, De Smet C, Godelaine D, Lethe B;
PI Lucas S;
XX
DR WPI; 1998-427951/36.
DR P-PSDB; AAW69663.
XX
PT New isolated LAGE-1 tumour associated nucleic acids - used to
PT develop products for the diagnosis and treatment of LAGE-1
PT associated disorders, particularly tumours
XX
PS Claim 1; Page 50-52; 73pp; English.
XX
CC The present sequence encodes LAGE-1 tumour associated protein (TAP).
CC The present invention also describes: (1) a method for treating a
CC subject with a disorder characterised by expression of a LAGE 1 nucleic
CC acid molecule or an expression product, comprising administering to the
CC subject autologous cytolytic T cells to ameliorate the disorder, where
CC the cytolytic T cells are specific for complexes of an HLA molecule and
CC a LAGE-1 TAP or an immunogenic fragment; (2) a method for treating a
CC subject with a disorder characterised by expression of a LAGE-1 nucleic
CC acid molecule or an expression product, comprising administering a
CC LAGE-1 TAP or an immunogenic fragment to ameliorate the disorder; and
CC (3) a method for selectively enriching a population of T cells with
CC cytolytic T cells specific for a LAGE-1 TAP comprising contacting an
CC isolated population of T cells with an agent presenting a complex of a
CC LAGE TAP or an immunogenic fragment and a HLA presenting molecule to
CC selectively enrich the isolated population of T cells with the cytolytic
CC T cells. The methods and products from the present invention can be used
CC for the diagnosis and treatment of LAGE-1 associated disorders,
CC particularly tumours.
XX
SQ Sequence 1002 BP; 179 A; 302 C; 336 G; 185 T; 0 other;

Query Match 100.0%; Score 248; DB 19; Length 1002;
Best Local Similarity 100.0%; Pred. No. 6.2e-114;
Matches 248; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagctttcctgttgatgtggatcacgcagtgcttttctgcccgtgttttttggctcaggct 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 756 cagctttcctgttgatgtggatcacgcagtgcttttctgcccgtgttttttggctcaggct 815

Qy 61 ccctcaggqcagaggcgctaaqcccaqcctqqcqcccctttcctaqqtcatqcctcctccc 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 816 ccctcaggqcagaggcgctaaqcccaqcctqqcqcccctttcctaqqtcatqcctcctccc 875

Qy 121 ctaqqgaatqqtcccaqcacqaqtqqccaqttcattqtqqqqqcctqattqtttatqcqct 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 876 ctaqqgaatqqtcccaqcacqaqtqqccaqttcattqtqqqqqcctqattqtttatqcqct 935

Qy 181 qqaqqaqqacqqcttacatqtttqtttctqtaqaaaataaaqctqaqctacqattccq 238
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 936 qqaqqaqqacqqcttacatqtttqtttctqtaqaaaataaaqctqaqctacqattccq 993

RESULT 2
AAD00149
ID AAD00149 standard; cDNA; 679 BP.
XX
AC AAD00149;
XX
DT 31-JUL-2000 (first entry)
XX
DE Human CTL-recognised Antigen on MELanoma (CAMEL) protein encoding cDNA.
XX
KW CAMEL; CTL-recognised Antigen on MELanoma; cytotoxic T lymphocyte; CTL;
KW tumour-associated antigen; LAGE 1; NY ESO 1; anticancer; melanoma; human;
KW cancer; immunotherapy; immune response; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT 5'UTR 1..9
FT /*tag = a
FT CDS 10..339
FT /*tag = b
FT /product= "Human CAMEL protein"
FT /note= "Tumour-associated antigen"
FT 3'UTR 340..679
FT /*tag = c
XX
PN WO200024758-A1.
XX
PD 27-APR-2000.
XX
PF 15-OCT-1999; 99WO-EP07832.
XX
PR 16-OCT-1998; 98EP-0119583.
XX
PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
PA (UYBO) UNIV HOSPITAL LEIDEN.
XX
PI Schrier PI, Aarnoudse CA, Heider K, Klade C;
XX
DR WPI; 2000-339685/29.
DR P-PSDB; AAY70854.
XX
PT Tumor associated antigen useful for cancer immunotherapy is encoded by
PT the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA
XX
PS Claim 12; Page 54; 73pp; English.
XX
CC The present sequence is the 4H8 cDNA clone of a tumour associated antigen
CC CAMEL (Cytotoxic T lymphocytes (CTL) recognised Antigen on MELanoma). It
CC is encoded by the open reading frame (ORF)-1 of LAGE-1 gene, a tumour
CC specific antigen. The 4H8 cDNA clone lacks the first 84 bp of the LAGE-1
CC cDNA and shows strong homology with NY-ESO-1, a melanoma specific tumour
CC antigen. The tumour-associated antigen displayed on melanoma cells is
CC recognised by cytotoxic T lymphocytes. CAMEL is expressed in tumour cell
CC lines, tumour tissues (e.g. breast and lung) and in restricted number of
CC healthy tissues. This sequence has anticancer activity. CAMEL tumour
CC antigen and immunogenic peptides derived from it are useful for cancer
CC immunotherapy. They have the potential to induce an immune response, by
CC eliciting a CTL response. The DNA molecule is used for construction of
CC recombinant or fusion proteins.
XX
SQ Sequence 679 BP; 120 A; 208 C; 221 G; 130 T; 0 other;

Query Match 97.9%; Score 234; DB 21; Length 679;
Best Local Similarity 100.0%; Pred. No. 2.4e-111;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagctttcctgttgatgtggatcacgcagtgcttttctgcccgtgttttttggctcaggct 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 432 cagctttcctgttgatgtggatcacgcagtgcttttctgcccgtgttttttggctcaggct 491

Qy 61 ccctcaggqcagaggcgctaaqcccaqcctqqcqcccctttcctaqqtcatqcctcctccc 120
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 492 ccctcaggqcagaggcgctaaqcccaqcctqqcqcccctttcctaqqtcatqcctcctccc 551

Qy 121 ctaqqgaatqqtcccaqcacqaqtqqccaqttcattqtqqqqqcctqattqtttatqcqct 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 552 ctaqqgaatqqtcccaqcacqaqtqqccaqttcattqtqqqqqcctqattqtttatqcqct 611

Qy 181 qqaqqaqqacqqcttacatqtttqtttctqtaqaaaataaaqctqaqctacqattccq 238
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 612 qqaqqaqqacqqcttacatqtttqtttctqtaqaaaataaaqctqaqctacqattccq 671

RESULT 3
AAV50447
ID AAV50447 standard; cDNA; 755 BP.
XX
AC AAV50447;
XX

```
DT   27-OCT-1998  (first entry)
XX
DE   Human LAGE 1 clone 4 nucleotide sequence
XX
KW   Human; LAGE 1; tumour associated protein; LL 1; diagnosis; tumour; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             53..595
FT                   /*tag=  a
FT                   /product= "LAGE 1"
XX
PN   WO9832855-A1.
XX
PD   30-JUL-1998.
XX
PF   27-JAN-1998;   98WO-US01445.
XX
PR   27-JAN-1997;   97US-0791495
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Boon-Falleur T,  De Smet C,  Godelaine D,  Lethe B;
PI   Lucas S;
XX
DR   WPI; 1998-427951/36.
DR   P-PSDB; AAW69664.
XX
PT   New isolated LAGE 1 tumour associated nucleic acids - used to
PT   develop products for the diagnosis and treatment of LAGE-1
PT   associated disorders, particularly tumours
XX
PS   Claim 1; Page 53-54; 73pp; English.
XX
CC   The present sequence encodes LAGE-1 tumour associated protein (TAP).
CC   The present invention also describes: (1) a method for treating a
CC   subject with a disorder characterised by expression of a LAGE-1 nucleic
CC   acid molecule or an expression product, comprising administering to the
CC   subject autologous cytolytic T cells to ameliorate the disorder, where
CC   the cytolytic T cells are specific for complexes of an HLA molecule and
CC   a LAGE-1 TAP or an immunogenic fragment; (2) a method for treating a
CC   subject with a disorder characterised by expression of a LAGE-1 nucleic
CC   acid molecule or an expression product, comprising administering a
CC   LAGE-1 TAP or an immunogenic fragment to ameliorate the disorder; and
CC   (3) a method for selectively enriching a population of T cells with
CC   cytolytic T cells specific for a LAGE-1 TAP comprising contacting an
CC   isolated population of T cells with an agent presenting a complex of a
CC   LAGE TAP or an immunogenic fragment and a HLA presenting molecule to
CC   selectively enrich the isolated population of T cells with the cytolytic
CC   T cells. The methods and products from the present invention can be used
CC   for the diagnosis and treatment of LAGE-1 associated disorders,
CC   particularly tumours.
XX
SQ   Sequence 755 BP; 126 A; 234 C; 252 G; 143 T; 0 other;

  Query Match             97.9%;  Score 233;  DB 19;  Length 755;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-111;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgttttggctcaggct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        515 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgttttggctcaggct 574

Qy         61 ccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatgcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        575 ccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatgcctcctccc 634

Qy        121 ctaggggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        635 ctaggggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 694

Qy        181 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagct-acga 233
              |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        695 ggaggaggacggcttacatgtttgtttctgtagaaaataaagctgagct-acga 747


RESULT   4
AAD00150
ID   AAD00150 standard; cDNA; 767 BP.
XX
AC   AAD00150;
XX
DT   31-JUL-2000  (first entry)
XX
DE   Human LAGE-1 splice variant, LAGE 1s encoding cDNA.
XX
KW   LAGE-1s; splice variant; CAMEL; CTL recognised Antigen on MELanoma; CTL;
KW   cytotoxic T lymphocyte; tumour associated antigen; NY-ESO-1; antigen; ss;
KW   human; cancer; melanoma; immunotherapy; immune response; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..53
FT                   /*tag=  a
FT   CDS             54..596
FT                   /*tag=  b
FT                   /product= "Human LAGE 1s protein"
FT                   /note= "Splice variant of LAGE 1"
FT   3'UTR           597..767
FT                   /*tag=  c
XX
PN   WO200023584-A1.
XX
PD   27-APR-2000.
XX
PF   15-OCT-1999;   99WO-EP07832.
XX
PR   16-OCT-1998;   98EP-0119583.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (UYLE-) UNIV HOSPITAL LEIDEN.
XX
PI   Schrier PI,  Aarnoudse CA,  Heider K,  Klade C;
XX
DR   WPI; 2000-339685/29.
DR   P-PSDB; AAY70860.
XX
PT   Tumor-associated antigen useful for cancer immunotherapy, is encoded by
PT   the open reading frame of LAGE 1 (a tumor specific antigen) cDNA
XX
PS   Example 1; Page 56-57; 73pp; English.
XX
CC   The present sequence is the cDNA encoding human LAGE-1 splice variant,
CC   LAGE 1s, a tumour specific antigen. It decodes the LAGE 1s protein from
CC   open reading frame-3 (ORF) and the CAMEL protein (Cytotoxic T lymphocytes
CC   (CTL)-recognised Antigen on MELanoma) from ORF 1. The LAGE 1(s/l) protein
CC   from ORF 1 is identical to the CAMEL protein. LAGE 1 is not expressed in
CC   healthy tissues except in testis and placenta. It also shows homology
CC   with the NY-ESO-1, a melanoma specific tumour antigen. The tumour
CC   associated antigen displayed on melanoma cells is recognised by cytotoxic
CC   T lymphocytes. This sequence has anticancer activity. CAMEL tumour
CC   antigen and immunogenic peptides derived from it are useful for cancer
CC   immunotherapy. They have the potential to induce an immune response, by
CC   eliciting a CTL response. The DNA molecule is used for the construction
CC   of recombinant or fusion proteins.
XX
SQ   Sequence 767 BP; 138 A; 234 C; 252 G; 143 T; 0 other;

  Query Match             97.9%;  Score 233;  DB 21;  Length 767;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-111;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy       1 cagctttcccctgttgatgtgcaatcacgcagtgcttttctgcccctgtttttgqctcaggct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     516 cagctttcccctgttgatgtgcaatcacgcagtgctttctgcccctgtttttgqctcaggct 575

Qy      61 cctcaqqqcaqaqqcqctaaqcccaqcctgqcqcccttcctaqgtcatqcctcctccc 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 cctcaqqqcaqaqqcqctaaqcccaqcctgqcqcccttcctaqgtcatqcctcctccc 635

Qy     121 ctaqqqaatqqtcccaqcacqaqtqqccaqttcattqtqqqqqcctqattqtttqtqqct 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 ctaqqqaatqqtcccaqcacqaqtqqccaqttcattqtqqqqqcctqattqtttqtqqct 695

Qy     181 qqaqqaqqqacqqcttacatqtttqtttctqtaqaaaataaaqctqaqctacqa 234
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     696 qqaqqaqqqacqqcttacatqtttqtttctqtaqaaaataaaqctqaqctacqa 748


RESULT   5
AAD00151
ID   AAD00151 standard; cDNA; 993 BP.
XX
AC   AAD00151;
XX
DT   31-JUL-2000  (first entry)
XX
DE   Human LAGE-1 unspliced variant, LAGE-1l encoding cDNA.
XX
KW   LAGE-1l; CAMEL; CTL-recognised Antigen on MELanoma; human; cancer; CTL;
KW   cytotoxic T lymphocyte; tumour-associated antigen; NY-ESO-1; anticancer;
KW   melanoma; immunotherapy; immune response; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..55
FT                   /*tag= a
FT   CDS             56..688
FT                   /*tag= b
FT                   /product= "Human LAGE 1l protein"
FT                   /note= "Unspliced variant of LAGE 1"
FT   3'UTR           689..993
FT                   /*tag= c
XX
PN   WO200023584-A1.
XX
PD   27-APR-2000.
XX
PF   15-OCT-1999;   99WO-EP07832.
XX
PR   16-OCT-1998;   98EP-0119583.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (UYBC-) UNIV HOSPITAL LEIDEN.
XX
PI   Schrier PI, Aarnoudse CA, Heider K, Blade C;
XX
DR   WPI; 2000-339685/29
DR   P-PSDB; AAY70861.
XX
PT   Tumor-associated antigen useful for cancer immunotherapy is encoded by
PT   the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA
XX
PS   Example 1; Page 58-59; 72pp; English.
XX
CC   The present sequence is the cDNA encoding human LAGE 1 unspliced variant,
CC   LAGE-1l, a tumour-specific antigen. It decodes the LAGE 1l protein from
CC   open reading frame-3 (ORF) and the CAMEL protein (Cytotoxic T lymphocytes
CC   (CTL)-recognised Antigen on MELanoma) from ORF-1. The LAGE-1(s/l) protein
CC   from ORF-1 is identical to the CAMEL protein. LAGE 1 is not expressed in
CC   healthy tissues except in testis and placenta. It also shows homology
CC   with the NY-ESO-1, a melanoma specific tumour antigen. The tumour-
CC   associated antigen displayed on melanoma cells is recognised by cytotoxic
CC   T lymphocytes. This sequence has antivancer activity. CAMEL tumour
CC   antigen and immunogenic peptides derived from it are useful for cancer
CC   immunotherapy. They have the potential to induce an immune response by
CC   eliciting a CTL response. The DNA molecule is used for the construction
CC   of recombinant or fusion proteins.
XX
SQ   Sequence 993 BP; 184 A; 295 C; 334 G; 180 T; 0 other;


  Query Match             97.9%;  Score 233;  DB 21;  Length 993;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-111;
  Matches  233;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       1 cagctttcccctgttgatgtgcaatcacgcagtgcttttctgcccctgtttttgqctcaggct 60
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     747 cagctttcccctgttgatgtgcaatcacgcagtgctttctgcccctgtttttgqctcaggct 806

Qy      61 cctcaqqqcaqaqqcqctaaqcccaqcctqqcqcccttcctaqgtcatqcctcctccc 120
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     807 cctcaqqqcaqaqqcqctaaqcccaqcctqqcqcccttcctaqgtcatqcctcctccc 866

Qy     121 ctaqqqaatqqtcccaqcacqaqtqqccaqttcattqtqqqqqcctqattqtttqtqqct 180
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     867 ctaqqqaatqqtcccaqcacqaqtqqccaqttcattqtqqqqqcctqattqtttqtqqct 926

Qy     181 qqaqqaqqqacqqcttacatqtttqtttctqtaqaaaataaaqctqaqctacqa 234
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     927 qqaqqaqqqacqqcttacatqtttqtttctqtaqaaaataaaqctqaqctacqa 979


RESULT   6
AAV38566
ID   AAV38566 standard; DNA; 752 BP.
XX
AC   AAV38566;
XX
DT   17-SEP-1998  (first entry)
XX
DE   DNA encoding a cancer associated antigen.
XX
KW   Cancer associated antigen; NY-ESO-1; regression; progression; ds;
KW   cancer; treatment; diagnosis; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             54..596
FT                   /*tag= a
FT                   /product= "cancer associated antigen
XX
PN   WO9814464-A1.
XX
PD   09-APR-1998.
XX
PF   19-SEP-1997;   97WO-US16335.
XX
PR   04-OCT-1996;   96US-0725182.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Chen Y, Jrijthout JW, Gure A, Jager E, Knuth A;
PI   Old LJ, Scanlan M;
XX
DR   WPI; 1998-286117/25.
DR   P-PSDB; AAW62584.
XX
PT   New isolated cancer associated antigen - is used to develop Ab's
PT   for the diagnosis and treatment of cancers and for monitoring cancer
PT   therapy
XX
PS   Claim 1; Fig 3; 49pp; English.
XX
CC   The present sequence encodes a cancer associated antigen. The clone
CC   from which the DNA sequence is obtained is designated LNY-1S. The
```

```
CC   specification described a method for determining regression, progression
CC   of onset of a cancerous condition, comprising monitoring a sample from a
CC   patient with the cancerous condition for a parameter selected from
CC   NY ESO 1 protein, a peptide derived from NY ESO 1 protein and cytolytic
CC   T cells specific for the peptide and an MHC molecule with which it
CC   non-covalently complexes. Methods for the treatment of a cancerous
CC   condition are also described. The NY ESO-1 protein and peptides derived
CC   from it can be used for diagnosis and treatment of cancers and to monitor
CC   the efficacy of a therapeutic regime.
XX
SQ   Sequence 752 BP; 126 A; 230 C; 256 G; 140 T; 0 other;

  Query Match             71.4%;  Score 170;  DB 19;  Length 752;
  Best Local Similarity   99.5%;  Pred. No. 1e-78;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtatttttggctcagct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db      516 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcagct 575

Qy       61 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      576 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctccc 635

Qy      121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      636 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 695

Qy      181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
              |||||||||||||||||||||||||||||||||||||||||
Db      696 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 736


RESULT 7
AAA61483
ID   AAA61483 standard; cDNA; 752 BP.
XX
AC   AAA61483;
XX
DT   23-OCT-2000  (first entry)
XX
DE   cDNA encoding human oesophageal cancer associated antigen NY ESO 1.
XX
KW   oesophageal cancer associated antigen; NY-ESO-1; human;
KW   immunogen; oesophageal carcinoma; melanoma; ovary; testis;
KW   transmembrane domain; antibody; diagnostic marker; drug delivery target;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             54..596
FT                   /*tag=  a
FT                   /product= "Oesophageal cancer associated antigen,
FT                             NY ESO 1"
FT   misc_feature    54..600
FT                   /*tag=  b
FT                   /note= "Nucleotides 54-600 are specifically claimed"
XX
PN   US6069233-A.
XX
PD   30-MAY-2000.
XX
PF   26-JAN-1998;   98US-0013150.
XX
PR   03-OCT-1996;   96US-0725381.
XX
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
PA   (CORR ) CORNELL RES FOUND INC.
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Scanlan M,  Gure AO,  Chen Y,  Latecl O,  Sahin U,  Pfreundschuh M;
PI   Old LJ;
XX
DR   WPI; 2000-410886/35.
DR   P-PSDB; AAB03154.
XX
PT   New isolated esophageal cancer-associated antigen useful as markers for
PT   producing antibodies and as targets for identifying abnormal
PT   conditions, e.g. infections and cancer
XX
PS   Claim 1; Fig 3; 9pp; English.
XX
CC   This sequence represents cDNA encoding a human oesophageal cancer
CC   associated antigen, NY-ESO 1. This sequence was isolated from a
CC   cDNA library prepared from a specimen of well to moderately
CC   differentiated squamous cell cancer of the oesophagus. Expression
CC   analysis demonstrated that NY ESO 1 was expressed in oesophageal
CC   carcinoma, certain melanoma cell lines and in normal ovary and testis
CC   tissue, but not in normal colon, kidney, liver or brain tissue. Analysis
CC   of the amino acid sequence of the protein indicates that the protein has
CC   a transmembrane domain, several N-myristoylation sites and
CC   O-phosphorylation sites and that it contains antigenic sequences in the
CC   N-terminal half of the protein. The antigen is useful as an immunogen
CC   when combined with an adjuvant, in both precursor and post
CC   translationally modified forms, and may be used to generate anti NY ESO
CC   antibodies. It can also be used as a diagnostic marker for oesophageal
CC   cancer, and can be utilised as a marker for the targetted delivery of
CC   therapeutic agents to oesophageal cancer cells. It can also be used to
CC   generate diagnostic or therapeutic agents.
XX
SQ   Sequence 752 BP; 126 A; 230 C; 256 G; 140 T; 0 other;

  Query Match             71.4%;  Score 170;  DB 21;  Length 752;
  Best Local Similarity   99.5%;  Pred. No. 1e-78;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy        1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtatttttggctcagct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db      516 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcagct 575

Qy       61 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      576 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctccc 635

Qy      121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      636 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 695

Qy      181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
              |||||||||||||||||||||||||||||||||||||||||
Db      696 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 736


RESULT 8
AAD00152
ID   AAD00152 standard; cDNA; 752 BP.
XX
AC   AAD00152;
XX
DT   31-JUL-2000  (first entry)
XX
DE   Human tumour antigen, NY ESO 1 cDNA.
XX
KW   NY-ESO-1; CAMEL; CTL recognised Antigen on MELanoma; human; cancer; CTL;
KW   cytotoxic T lymphocyte; tumour associated antigen; TAA; antigen;
KW   melanoma; immunotherapy; immune response; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   5'UTR           1..53
FT                   /*tag=  a
FT   CDS             54..596
```

```
FT                   /*tag= b
FT                   /product= "Human NY-ESO-1 protein"
FT                   /note= "Derived from open reading frame (ORF)-1"
FT   3'UTR           597..752
FT                   /*tag= c
FT   5'UTR           1..93
FT                   /*tag= d
FT                   /note= "5' UTR of ORF-2"
FT   CDS             94..270
FT                   /*tag= e
FT                   /product= "Human NY ESO 1 short variant protein"
FT                   /note= "Derived from open reading frame (ORF)-2"
FT   3'UTR           271..752
FT                   /*tag= f
FT                   /note= "3' UTR of ORF-2"
XX
PN   WO200023584-A1.
XX
PD   27-APR-2000.
XX
PF   15-OCT-1999;    99WO-EP007832.
XX
PR   16-OCT-1998;    98EP-0119583.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH
PA   (OYHO-) UNIV HOSPITAL LEIDEN.
XX
PI   Schrier PI,  Aarnoudse CA,  Heider K,  Klade C;
XX
DR   WPI; 2000-339685/29.
DR   P-PSDB; AAY70862, AAY70863.
XX
PT   Tumor-associated antigen useful for cancer immunotherapy is encoded by
PT   the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA -
XX
PS   Example 1; Page 61-62; 73pp; English.
XX
CC   The present sequence is the cDNA encoding human NY-ESO-1, a tumour
CC   antigen, identified by screening a cDNA library of an oesophagus
CC   carcinoma. It has two different reading frames and the proteins decoded
CC   contain epitopes of tumour specific T cells. NY ESO 1 is expressed in
CC   different tumour types, but not in healthy tissues except in testis. It
CC   also shows homology with the CAMEL (Cytotoxic T lymphocyte (CTL)
CC   recognised Antigen on MELanoma) cDNA, a tumour-associated antigen. The
CC   tumour-associated antigen displayed on melanoma cells is recognised by
CC   cytotoxic T lymphocytes. This sequence has anticancer activity. CAMEL
CC   tumour antigen and immunogenic peptides derived from it are useful for
CC   cancer immunotherapy. They have the potential to induce an immune
CC   response, by eliciting a CTL response. The DNA molecule is used for the
CC   construction of recombinant or fusion proteins.
XX
SQ   Sequence 752 BP; 126 A; 230 C; 256 G; 140 T; 0 other;
```

```
  Query Match             71.4%;  Score 170;  DB 21;  Length 752;
  Best Local Similarity   99.5%;  Pred. No. 1e-78;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cagctttcctgttgatgtggatcacgcaatgctttctgcccgtgttttttggctcaggct  60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     516 cagctttcctgttgatgtggatcacgcaatgctttctgcccgtgttttttggctcaggct  575

Qy      61 ccctcagggcagaggcgctaagcccagcctgagcgcccttcctaagtcatgcctcctccc  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     576 ccctcagggcagaggcgctaagcccagcctgagcgcccttcctaagtcatgcctcctccc  635

Qy     121 ctaggaatgatccccagcacgagtgagccagttcattgtcgggagcctgattgtttgtcgct  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     636 ctaggaatgatccccagcacgagtgagccagttcattgtcgggagcctgattgtttgtcgct  695

Qy     181 gaggaggacgagcttacatgtttgtttctgtagaaaataaa 221
           |||||||||||||||||||||||||||||||||||||||||
Db     696 gaggaggacgagcttacatgtttgtttctgtagaaaataaa 736
```

```
RESULT   9
AAZ38480
ID   AAZ38480 Standard; cDNA; 752 BP.
XX
AC   AAZ38480;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Human tumour antigen NY-ESO-1 cDNA.
XX
KW   Cancer; tumour; antigen; MHC; major histocompatibility complex;
KW   T-cell; cytotoxic; helper; stimulation; proliferation; treatment;
KW   diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW   prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW   lymphoma; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             54..596
FT                   /*tag= a
FT                   /product= "Human tumour antigen NY ESO 1"
XX
PN   WO9953938-A1.
XX
PD   28-OCT-1999.
XX
PF   24-MAR-1999;    99WO-US06875.
XX
PR   17-APR-1998;    98US-0082422.
PR   02-OCT-1998;    98US-0165546.
XX
PA   (LUDW ) LUDWIG INST CANCER RES.
XX
PI   Stockert E,  Jager E,  Chen Y,  Scanlan M,  Alexander K,  [...];
PI   Gure A,  Ritter G;
XX
DR   WPI; 2000-038484/03.
DR   P-PSDB; AAY52430.
XX
PT   Novel peptides which bind to MHC class I and MHC class II molecules
PT   useful for therapeutic and diagnostic purposes -
XX
PS   Claim 30; Fig 7; 49pp; English.
XX
CC   This sequence represents cDNA encoding a human tumour antigen NY-ESO-1,
CC   which was isolated from an oesophagus squamous cell cancer cDNA
CC   library. Tissue localisation studies revealed it to be expressed at
CC   high levels in normal ovary and testis, but not in normal colon, kidney,
CC   liver, brain, oesophagus and skin. It was expressed in certain tumours
CC   and tumour cell lines with some degree of frequency; those included
CC   melanoma specimens and cell lines, and breast and bladder cancer
CC   specimens, with expression in other tumour types being sporadic.
CC   Peptides derived from NY ESO 1 are bound by both MHC (major
CC   histocompatibility complex) Class I and Class II molecules. The
CC   presentation to T cells, Peptides AAY52431 Y52434 bind to Class I HLA A2
CC   molecules, thereby stimulating proliferation of cytotoxic T cells, while
CC   peptides AAY52435 Y52440 bind to Class II HLA DR53 molecules, stimulating
CC   helper T-cell proliferation. The peptides derived from NY ESO 1 may be
CC   used in methods and compositions used for the treatment, diagnosis and
CC   prevention of cancers (such as melanoma, breast cancer, prostate cancer,
CC   lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC   or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ   Sequence 752 BP; 126 A; 230 C; 256 G; 140 T; 0 other;
```

```
  Query Match             71.4%;  Score 170;  DB 21;  Length 752;
  Best Local Similarity   99.5%;  Pred. No. 1e-78;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;
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```
Qy        1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcagct 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      516 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcagct 575

Qy       61 ccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatgcctcctcc 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      576 ccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatgcctcctcc 635

Qy      121 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      636 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 695

Qy      181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
            |||||||||||||||||||||||||||||||||||||||||
Db      696 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 736
```

```
RESULT 10
AAF58634
ID   AAF58634 standard; cDNA; 752 BP.
XX
AC   AAF58634;
XX
DT   27 APR 2001  (first entry)
XX
DE   Human NY ESO 1 nucleotide sequence.
XX
KW   Human; NY ESO 1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW   HLA A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW   non-small cell lung carcinoma; tumour status determination; ss.
XX
OS   Homo sapiens.
XX
PN   WO200107917-A1.
XX
PD   01 FEB 2001.
XX
PF   14 JUL 2000; 2000WO-US19220.
XX
PR   23 JUL 1999;   99US-0359503.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Jager E,  Stockert E,  Old LJ,  Knuth A,  Chen Y,  Scanlan M;
XX
DR   WPI; 2001 182822/18.
DR   P-PSDB; AAB69946.
XX
PT   Method useful for determining the status (e.g. progression, regression
PT   or stability of the disease) of a cancerous condition, involves
PT   determining the levels of NY-ESO-1 specific antibodies in a sample
PT   taken from a patient  -
XX
PS   Example 5; Fig 3; 50pp; English.
XX
CC   The present sequence encodes human NY ESO 1. It is provided in a
CC   specification relating to a method for determining the status of a
CC   cancerous condition in a patient with a tumour that expresses NY ESO-1.
CC   The method comprises assaying a sample taken from the patient for
CC   antibodies that specifically bind to the NY ESO-1 and comparing the
CC   value obtained to a prior value obtained from assay of a prior sample
CC   taken from the patient. Any difference between the values is indicative
CC   of a change in status of the cancerous condition. The method is useful
CC   for determining whether a cancerous condition is progressing, regressing
CC   or remaining stable, in particular in patients receiving treatment for a
CC   melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC   carcinoma.
XX
SQ   Sequence 752 BP; 126 A; 230 C; 256 G; 140 T; 0 other;
```

```
  Query Match             71.4%;  Score 1??;  DB 22;  Length ??;
  Best Local Similarity   99.5%;  Pred. No. 1e-78;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels   ?;  Gaps   ?;

Qy        1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcagct 60
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      516 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcagct 575

Qy       61 ccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatgcctcctcc 120
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      576 ccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatgcctcctcc 635

Qy      121 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 180
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      636 ctagggaatggtcccagcacgagtggccagttcattgtgggggcctgattgtttgtcgct 695

Qy      181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
            |||||||||||||||||||||||||||||||||||||||||
Db      696 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 736
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```
RESULT 11
AAV50348
ID   AAV50348 standard; cDNA; 755 BP.
XX
AC   AAV50348;
XX
DT   27 OCT 1998  (first entry)
XX
DE   Human NY ESO-1 nucleotide sequence, formerly known as LL 1.2 clone.
XX
KW   Human; LAGE-1; tumour associated protein; LL 1; diagnosis; tumour; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             51..593
FT                   /*tag=  a
FT                   /product= "NY ESO 1"
XX
PN   WO9832855-A1.
XX
PD   30-JUL-1998.
XX
PF   27-JAN-1998;   98WO-US01445.
XX
PR   27-JAN-1997;   97US-0791495.
XX
PA   (LUDW ) LUDWIG INST CANCER RES.
XX
PI   Boon-Falleur T,  De Smet C,  Godelaine D,  Lethe B,
PI   Lucas S;
XX
DR   WPI; 1998-427951/36.
DR   P-PSDB; AAW69665.
XX
PT   New isolated LAGE-1 tumour associated nucleic acid, used to
PT   develop products for the diagnosis and treatment of LAGE 1
PT   associated disorders, particularly tumours
XX
PS   Example 2; Page 56-57; 73pp; English.
XX
CC   The present sequence encodes human NY ESO 1, formerly known as LL 1.2
CC   clone, which is used in an example from the present invention which
CC   describes LAGE 1 tumour associated protein (TAP). The present invention
CC   also describes: (1) a method for treating a subject with a disorder
CC   characterised by expression of a LAGE 1 nucleic acid molecule or an
CC   expression product, comprising administering to the subject autologous
CC   cytolytic T cells to ameliorate the disorder, where the cytolytic T
CC   cells are specific for complexes of an HLA molecule and a LAGE 1 TAP or
CC   an immunogenic fragment; (2) a method for treating a subject with a
CC   disorder characterised by expression of a LAGE 1 nucleic acid molecule
CC   or an expression product, comprising administering a LAGE 1 TAP or an
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CC   immunogenic fragment to ameliorate the disorder; and (3) a method for
CC   selectively enriching a population of T cells with cytolytic T cells
CC   specific for a LAGE-1 TAP comprising contacting an isolated population
CC   of T cells with an agent presenting a complex of a LAGE TAP or a
CC   immunogenic fragment and a HLA presenting molecule to selectively
CC   enrich the isolated population of T cells with the cytolytic T cells.
CC   The methods and products from the present invention can be used for the
CC   diagnosis and treatment of LAGE-1 associated disorders, particularly
CC   tumours.
XX
SQ   Sequence 755 BP; 131 A; 229 C; 256 G; 139 T; 0 other;


  Query Match             71.4%;  Score 170;  DB 17;  Length 755;
  Best Local Similarity   99.5%;  Pred. No. 1e-78;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cagcttteeetqttqatqtqqatcaeqcaqtqcttctqcccqtqttttqqctcaqcct 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     513 cagctttccctgttgatgtggatcacgcagtgcttctgcccgtgttttggctcagcct 572

Qy      61 cctctcaqqqcaqaggcgctaaqcccaqcctqqcqccctttctaqqtcatqcctcctcc 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     573 cctctcaqqqcaqaggcgctaaqcccaqcctqqcqccctttctaqqtcatqcctcctcc 632

Qy     121 ctaqqqaatqqtcccaqcacqaqtqqccaqttcattqtqqqqcctqattqtttqtqcct 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     633 ctaqqqaatqqtcccaqcacqaqtqqccaqttcattqtqqqqcctqattqtttqtqcct 692

Qy     181 qqaqqaqqacqqcttacatqtttqtttctqtaqaaaataaa 221
           |||||||||||||||||||||||||||||||||||||||||
Db     693 qqaqqaqqacqqcttacatqtttqtttctqtaqaaaataaa 733


RESULT  12
AAX58599
ID   AAX58599 standard; cDNA; 806 BP.
XX
AC   AAX58599;
XX
DT   16-AUG-1999  (first entry)
XX
DE   Human cancer antigen NY ESO-1/CAG-3 cDNA.
XX
KW   NY ESO 1/CAG 3 gene; CAG 3 gene, cancer antigen, human, leukaemia;
KW   non-Hodgkin's lymphoma, Hodgkin's lymphoma, lung cancer;
KW   metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW   uterine cancer; breast cancer, prostate cancer, ovarian cancer,
KW   cervical cancer, bladder cancer, kidney cancer; pancreatic cancer;
KW   liver cancer, sarcoma, tumour, diagnosis, immunotherapy, therapy,
KW   vaccine; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             89..631
FT                   /*tag= a
FT                   /product= "CAG-3" (claim 1 in Claim 2), encodes AAY05965"
FT   CDS             129..305
FT                   /*tag= b
FT                   /note= "ORF2 (claimed in Claim 4), encodes AAY05966"
XX
PN   WO9918206-A2.
XX
PD   15-APR-1999.
XX
PF   21-SEP-1998;   98WO-US19609.
XX
PR   08-OCT-1997;   97US-0061428.
XX
PA   (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI   Rosenberg SA, Wang RF;
XX
DR   WPI; 1999-277270/23.
DR   P-PSDB; AAY05965, AAY05966.
XX
PT   Cancer antigen NY ESO1/CAG-3
XX
PS   Claim 1; Fig 3A; 88pp; English.
XX
CC   This is the nucleotide sequence of a cDNA clone that encodes a novel
CC   human cancer antigen, termed NY ESO 1/CAG 3 (or CAG-3). The clone
CC   was isolated from a melanoma cell line 586mel library. CAG-3 is
CC   a new and potent tumour antigen capable of eliciting an antigen
CC   specific immune response by T cells. Cancer peptides encoded by
CC   ORF 1 or ORF-2 of the CAG-3 gene, and their variants (see AAY 5[illegible]
CC   are useful as cancer vaccines that protect the recipient from
CC   [illegible] cancer. The invention provides vectors that include
CC   DNA encoding a CAG 3 cancer peptide, and transfected or transduced
CC   host cells. These cells and host cells can serve as vaccines in
CC   which expression of a cancer peptide results in stimulation of tumour
CC   antigen specific T cells in an immunised mammal. The invention also
CC   provides: a method of diagnosis of cancer or precancer; a transgenic
CC   animal, antisense oligonucleotides that inhibit expression of the
CC   cancer peptide or tumour antigen; antibodies reacting with the CAG-3
CC   cancer peptide, useful in diagnostic and detection assays; and
CC   methods for preventing or inhibiting cancer by administering a
CC   cancer peptide, with or without an HLA molecule. The cancer
CC   peptides form part of, or are derived from, cancers such as primary
CC   or metastatic melanoma, thymoma, lymphoma, sarcoma, lung cancer,
CC   liver cancer, leukaemia, uterine cancer, cervical cancer, bladder
CC   cancer, kidney cancer and adenocarcinomas such as breast, prostate,
CC   ovarian, pancreatic and thyroid cancers. Melanoma is treated by
CC   inducing cancer specific T cells in vitro for subsequent return to
CC   a patient.
XX
SQ   Sequence 806 BP; 155 A; 247 C; 269 G; 145 T; 0 other;


  Query Match             71.4%;  Score 170;  DB 20;  Length 806;
  Best Local Similarity   99.5%;  Pred. No. 1e-78;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 cagcttteeetqttqatqtqqatcaeqcaqtqcttctqcccqtqttttqqctcaqcct 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     551 cagctttccctgttgatgtggatcacgcagtgcttctgcccgtgttttggctcagcct 610

Qy      61 cctctcaqqqcaqaggcgctaaqcccaqcctqqcqccctttctaqqtcatqcctcctcc 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     611 cctctcaqqqcaqaggcgctaaqcccaqcctqqcqccctttctaqqtcatqcctcctcc 670

Qy     121 ctaqqqaatqqtcccaqcacqaqtqqccaqttcattqtqqqqcctqattqtttqtqcct 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     671 ctaqqqaatqqtcccaqcacqaqtqqccaqttcattqtqqqqcctqattqtttqtqcct 730

Qy     181 qqaqqaqqacqqcttacatqtttqtttctqtaqaaaataaa 221
           |||||||||||||||||||||||||||||||||||||||||
Db     731 qqaqqaqqacqqcttacatqtttqtttctqtaqaaaataaa 771


RESULT  13
AAV50349
ID   AAV50349 standard; cDNA; 217 BP.
XX
AC   AAV50349;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Human LAGE-1 clone 1 nucleotide sequence.
XX
KW   Human; LAGE-1; tumour associated protein; LL 1; diagnosis; tumours; ds.
XX
OS   Homo sapiens.
XX
PN   WO9842855-A1.
```

XX
PD 30-JUL-1998.
XX
PF 27-JAN-1998; 98WO-US01445.
XX
PR 27-JAN-1997; 97US-0791495.
XX
PA (LUDW) LUDWIG INST CANCER RES.
XX
PI Boon Fallour T, De Smet C, Godelaine D, Lethe B;
PI Lucas S;
XX
DR WPI; 1998-427961/36.
XX
PT New isolated LAGE-1 tumour associated nucleic acids used to
PT develop products for the diagnosis and treatment of LAGE 1
PT associated disorders, particularly tumours
XX
PS Example 1; Page 49; 74pp; English.
XX
CC The present sequence represents LAGE 1 clone 1 from the present
CC invention which describes LAGE 1 tumour associated protein (TAP).
CC The present invention also describes: (1) a method for treating a
CC subject with a disorder characterised by expression of a LAGE-1 nucleic
CC acid molecule or an expression product, comprising administering to the
CC subject autologous cytolytic T cells to ameliorate the disorder, where
CC the cytolytic T cells are specific for complexes of an HLA molecule and
CC a LAGE-1 TAP or an immunogenic fragment; (2) a method for treating a
CC subject with a disorder characterised by expression of a LAGE-1 nucleic
CC acid molecule or an expression product, comprising administering a
CC LAGE 1 TAP or an immunogenic fragment to ameliorate the disorder; and
CC (3) a method for selectively enriching a population of T cells with
CC cytolytic T cells specific for a LAGE-1 TAP comprising contacting an
CC isolated population of T cells with an agent presenting a complex of a
CC LAGE TAP or an immunogenic fragment and a HLA presenting molecule to
CC selectively enrich the isolated population of T cells with the cytolytic
CC T cells. The methods and products from the present invention can be used
CC for the diagnosis and treatment of LAGE 1 associated disorders,
CC particularly tumours.
XX
SQ Sequence 217 BP; 48 A; 72 C; 53 G; 44 T; 0 other;

Query Match 10.1%; Score 24; DB 19; Length 217;
Best Local Similarity 100.0%; Pred. No. 0.0044;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 cagcttcccctgttgatgtggatc 24
||||||||||||||||||||||||
Db 194 cagcttcccctgttgatgtggatc 217

RESULT 14
AAX58604/c
ID AAX58604 standard; DNA; 22 BP.
XX
AC AAX58604;
XX
DT 16-APR-1999 (first entry)
XX
DE Human cancer antigen NY ESO-1/CAG-3 primer ES0-P5.
XX
KW NY ESO-1/CAG-3 gene; CAG-3 gene; cancer peptide; antigen; human;
KW leukaemia; non-Hodgkins lymphoma; Hodgkins lymphoma; lung cancer;
KW metastasis; melanoma; adenocarcinoma; thymoma; colon cancer;
KW uterine cancer; breast cancer; prostate cancer; ovarian cancer;
KW cervical cancer; bladder cancer; kidney cancer; pancreatic cancer;
KW liver cancer; sarcoma; tumour; diagnosis; immunotherapy; therapy;
KW vaccine; PCR; primer; ss.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN WO9918209-A2.
XX
PD 15-APR-1999.
XX
PF 21-SEP-1998; 98WO-US19609.
XX
PR 08-OCT-1997; 97US-0061428.
XX
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Rosenberg SA, Wang RF;
XX
DR WPI; 1999-277239/23.
XX
PT Cancer antigen NY ESO1/CAG-3
XX
PS Example 1; Page 32; 88pp; English.
XX
CC Primer ES0-P5 and primer ES0-P2 (see AAX58603) were used in PCR
CC PCR amplification of human ES0-1/CAG-3 cDNA sequences obtained from
CC total RNA extracted from tumour cell lines. Cancer peptides
CC derived from CAG-3, portions of them and their variants (see
CC AAY05965-87), are useful as cancer vaccines that protect against
CC cancer. The cancer peptides form part of, or are derived
CC from, cancers such as primary or metastatic melanoma, thymoma,
CC lymphoma, sarcoma, lung cancer, liver cancer, leukaemia, uterine
CC cancer, cervical cancer, bladder cancer, kidney cancer and
CC adenocarcinomas such as breast, prostate, ovarian, pancreatic and
CC thyroid cancers.
XX
SQ Sequence 22 BP; 5 A; 10 C; 4 G; 3 T; 0 other;

Query Match 9.2%; Score 22; DB 20; Length 22;
Best Local Similarity 100.0%; Pred. No. 0.048;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 174 tgtcgctgcgaggagcgacggctt 195
|||||||||||||||||||||||
Db 22 TGTCGCTGCGAGGAGCGACGGCTT 1

RESULT 15
AAD00156/c
ID AAD00156 standard; DNA; 21 BP.
XX
AC AAD00156;
XX
DT 31-JUL-2000 (first entry)
XX
DE Reverse PCR primer B2, for construction of pCR 464 cont 1.
XX
KW CAMEL; CTL recognised Antigen on MELanoma; cytotoxic T lymph [illegible]
KW tumour associated antigen; LAGE 1; NY ESO 1; anti-cancer; melanoma, breast
KW cancer; immunotherapy; immune response; PCR primer; ss.
XX
OS Homo sapiens.
XX
PN WO200025584-A1.
XX
PD 27-APR-2000.
XX
PF 19-OCT-1999; 99WO-EP007852.
XX
PR 16-OCT-1998; 98EP-0119583.
XX
PA (BOER) B BOEHRINGER INGELHEIM INT GMBH.
PA (GYBO-) UNIV HOSPITAL LEIDEN.
XX
PI Schrier PI, Aarnoudse CA, Boelder K, Klade C;
XX
DR WPI; 2000-338985/29.
XX

```
PT   Tumor-associated antigen useful for cancer immunotherapy is encoded by
PT   the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA -
XX
PS   Disclosure; Page 66; 73pp; English.
XX
CC   The present DNA sequence is the reverse PCR primer R2, used along with
CC   forward PCR primer SP6F-pSV, to generate the deletion construct,
CC   pCR-464 of CAMEL cDNA clone 4H8.
CC   The tumour-associated antigen, CAMEL (Cytotoxic T lymphocytes (CTL)
CC   recognised Antigen on MELanoma) is encoded by the open reading frame
CC   (ORF)-1 of LAGE-1 gene, a tumour-specific antigen. It shows strong
CC   homology with NY ESO 1, a tumour specific antigen. The tumour-associated
CC   antigen displayed on melanoma cells is recognised by cytotoxic T
CC   lymphocytes. CAMEL is expressed in tumour cell lines, tumour tissues
CC   (e.g. breast and lung) and in restricted number of healthy tissues. It
CC   has anticancer activity. CAMEL tumour antigen and immunogenic peptides
CC   derived from it are useful for cancer immunotherapy. They have the
CC   potential to induce an immune response, by eliciting a CTL response. The
CC   DNA molecule is used for construction of recombinant or fusion proteins.
XX
SQ   Sequence 21 BP; 6 A; 7 C; 4 G; 4 T; 0 other;


  Query Match             8.8%;  Score 21;  DB 21;  Length 21;
  Best Local Similarity   100.0%;  Pred. No. 0.76;
  Matches   21;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      13 ttgatgtggatcacgcaagtgc 33
           |||||||||||||||||||||
Db      21 TTGATGTGGATCACGCAGTGC 1


RESULT  16
AAV38568/c
ID   AAV38568 standard; DNA; 42 BP.
XX
AC   AAV38568;
XX
DT   17-SEP-1998  (first entry)
XX
DE   PCR primer used to amplify DNA encoding a cancer associated antigen.
XX
KW   Cancer associated antigen; NY-ESO-1; regression; progression; onset;
KW   cancer; treatment; diagnosis; PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9814464 A1.
XX
PD   09-APR-1998.
XX
PF   15-SEP-1997;   97WO-US16435.
XX
PR   03-OCT-1996;   96US-0725182.
XX
PA   (LUDW-) LUDWIG INST CANCER RES
XX
PI   Chen Y,  Drijfhout JW,  Gure A,  Jager E,  Knuth A;
PI   Old LJ,  Scanlan M;
XX
DR   WPI; 1998-286417/25.
XX
PT   New isolated cancer associated antigen - is used to develop products
PT   for the diagnosis and treatment of cancers and for monitoring cancer
PT   therapy
XX
PS   Example 6; Page 12; 49pp; English.
XX
CC   PCR primers AAV38567-68 were used to amplify nucleotides 271 to 599
CC   of DNA encoding a cancer associated antigen (AAV38566). The clone
CC   from which the DNA sequence is obtained is designated NY-ESO-1. The
CC   specification described a method for determining regression, progression
CC   of onset of a cancerous condition, comprising monitoring a sample from a
CC   patient with the cancerous condition for a parameter selected from
CC   NY-ESO-1 protein, a peptide derived from NY ESO 1 protein and cytolytic
CC   T cells specific for the peptide and an MHC molecule with which it
CC   non-covalently complexes. Methods for the treatment of a cancerous
CC   condition are also described. The NY-ESO 1 protein and peptides derived
CC   from it can be used for diagnosis and treatment of cancers and to
CC   monitor the efficacy of a therapeutic regime.
XX
SQ   Sequence 42 BP; 6 A; 12 C; 7 G; 7 T; 0 other;


  Query Match             8.8%;  Score 20;  DB 19;  Length 42;
  Best Local Similarity   100.0%;  Pred. No. 0.52;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      65 cagggcagaggcgctaagcc 84
           ||||||||||||||||||||
Db      32 CAGGGCAGAGGCGCTAAGCC 13


RESULT  17
AAD00159/c
ID   AAD00159 standard; DNA; 32 BP.
XX
AC   AAD00159;
XX
DT   31-JUL-2000  (first entry)
XX
DE   LAGE 1 specific PCR primer, ESO 1B.
XX
KW   CAMEL CTL recognised Antigen on MELanoma; cytotoxic T lymphocyte; CTL;
KW   tumour-associated antigen; LAGE-1; NY-ESO-1; anticancer; melanoma; human;
KW   cancer; immunotherapy; immune response; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200037634-A1.
XX
PD   27-APR-2000.
XX
PF   15-OCT-1999;   99WO-EP07832.
XX
PR   16-OCT-1998;   98EP-0119583.
XX
PA   (BOEH ) BOEHRINGER INGELHEIM INT GMBH.
PA   (UYHO-) UNIV HOSPITAL LEIDEN.
XX
PI   Schrier PI,  Aarnoudse CA,  Heider K,  Klade C;
XX
DR   WPI; 2000-439585/29.
XX
PT   Tumor-associated antigen useful for cancer immunotherapy, is encoded by
PT   the open reading frame of LAGE-1 (a tumor-specific antigen) cDNA
XX
PS   Example 6; Page 67; 73pp; English.
XX
CC   The present DNA sequence is LAGE 1 specific PCR primer ESO 1B used in
CC   RT-PCR of LAGE-1 cDNA. It is used to determine the expression of LAGE 1
CC   or CAMEL protein in tumour tissues derived from breast and lung cancer.
CC   The tumour-associated antigen, CAMEL (Cytotoxic T lymphocytes (CTL)-
CC   recognised Antigen on MELanoma) is encoded by the open reading frame
CC   (ORF)-1 of LAGE 1 gene, a tumour-specific antigen. It shows strong
CC   homology with NY-ESO-1, a tumour specific antigen. The tumour-associated
CC   antigen displayed on melanoma cells is recognised by cytotoxic T
CC   lymphocytes. CAMEL is expressed in tumour cell lines, tumour tissues
CC   (e.g. breast and lung) and in restricted number of healthy tissues. It
CC   has anticancer activity. CAMEL tumour antigen and immunogenic peptides
CC   derived from it are useful for cancer immunotherapy. They have the
CC   potential to induce an immune response, by eliciting a CTL response. The
CC   DNA molecule is used for construction of recombinant or fusion proteins.
XX
SQ   Sequence 32 BP; 6 A; 12 C; 7 G; 7 T; 0 other;
```

```
  Query Match             8.4%;  Score 20;  DB 21;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0.52;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      65 cagggcagaggcgctaagcc 84
           ||||||||||||||||||||
Db      32 CAGGGCAGAGGCGCTAAGCC 13


RESULT  18
AAZ49179/c
ID   AAZ49179 standard; DNA; 32 BP.
XX
AC   AAZ49179;
XX
DT   13-APR-2000  (first entry)
XX
DE   PCR primer for NY-ESO-1 coding sequence.
XX
KW   SSX 2; SSX1 gene; breast cancer; melanoma; NY ESO 1; SCP 1; MAGE 3;
KW   diagnosis; detection; tumour rejection antigen precursor; PCR primer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200000642-A1.
XX
PD   06-JAN-2000.
XX
PF   03-JUN-1999;   99WO-US12294.
XX
PR   26-JUN-1998;   98US-0105907.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Sahin U,  Jungbluth A,  Chen Y,  Old LJ,  Pfreundschuh M;
XX
DR   WPI; 2000-137070/12.
XX
PT   Detecting breast cancer and melanoma used for diagnosis and in
PT   development of targeted therapy.
XX
PS   Claim 8; Page 5; 24pp; English.
XX
CC   This sequence represents a PCR primer for the NY-ESO-1 gene.
CC   The invention relates to a method for determining breast cancer or
CC   melanoma in a sample by assaying for expression of NY ESO 1, SSX 2 and
CC   SCP-1 for breast cancer, or NY-ESO 1, SSX 2 and MAGE-3 for melanoma, the
CC   expression of at least one is an indicator of possible breast cancer, and
CC   the expression of at least two is an indicator of possible melanoma. The
CC   method is used to diagnose breast cancer and melanoma, and to develop
CC   therapies, e.g. a mixture of peptides, derived from tumour antigens and
CC   known to associate with major histocompatibility complex to promote
CC   cytolytic T cell proliferation, can be prepared based on the determined
CC   pattern of antigen expression in a particular sample. Detecting two or
CC   more of the specified tumour rejection antigen precursors improves the
CC   accuracy of the assay.
XX
SQ   Sequence 32 BP; 6 A; 12 C; 7 G; 7 T; 0 other;


  Query Match             8.4%;  Score 20;  DB 21;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0.52;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      65 cagggcagaggcgctaagcc 84
           ||||||||||||||||||||
Db      32 CAGGGCAGAGGCGCTAAGCC 13


RESULT  19
AAZ38382/c
ID   AAZ38382 standard; DNA; 32 BP.
XX
AC   AAZ38382;
XX
DT   15-FEB-2000  (first entry)
XX
DE   Human tumour antigen NY ESO 1 reverse transcriptase (rt) primer #3
XX
KW   Cancer; tumour; antigen; MHC; major histocompatibility complex;
KW   T-cell; cytotoxic; helper; stimulation; proliferation; treatment;
KW   diagnosis; prevention; melanoma; breast cancer; ovarian cancer;
KW   prostate cancer; hepatoma; thyroid cancer; bladder cancer; lung cancer;
KW   lymphoma; reverse transcriptase(rt); RT PCR; primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9953938-A1.
XX
PD   28-OCT-1999.
XX
PT   24-MAR 1999;   99WO-US06875.
XX
PR   17-APR-1998;   98US-0062422.
PR   02-OCT-1998;   98US-0165546.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Stockert E,  Jager E,  Chen Y,  Scanlan M,  Alexander K    [+1];
PI   Gure A,  Ritter G;
XX
DR   WPI; 2000-038483/03.
XX
PT   Novel peptides which bind to MHC class I and MHC class II molecules
PT   useful for therapeutic and diagnostic purposes.
XX
PS   Example 6; Page 13; 49pp; English.
XX
CC   This sequence represents NY-ESO-1 reverse transcriptase PCR (RT PCR)
CC   primer #3, used with primer #2 (AAZ38381) in studies to ascertain
CC   whether RNAs encoding the human tumour antigen NY ESO 1 were
CC   expressed in melanoma cell lines and tumour samples. Tissue
CC   localisation studies also revealed it to be expressed at
CC   high levels in normal ovary and testis but not in normal colon, kidney,
CC   liver, brain, oesophagus and skin. It was expressed in certain lung and
CC   tumour cell lines with some degree of frequency, these included the
CC   melanoma specimens and cell lines, and breast and bladder cancer
CC   specimens, with expression in other tumour types being sporadic.
CC   Peptides derived from NY-ESO 1 are bound by both MHC (major
CC   histocompatibility complex) Class I and Class II molecules for
CC   presentation to T-cells. Peptides AAY52431-Y52444 bind to Class I HLA-A,
CC   molecules, thereby stimulating proliferation of cytotoxic T cells, while
CC   peptides AAY52435-Y52440 bind to Class II HLA DR53 molecules, stimulating
CC   helper T-cell proliferation. The peptides derived from NY-ESO 1 may be
CC   used in methods and compositions used for the treatment, diagnosis and
CC   prevention of cancers (such as melanoma, breast cancer, prostate cancer,
CC   lung cancer, hepatoma, ovarian cancer, thyroid cancer, bladder cancer,
CC   or lymphoma) and to stimulate the proliferation of T cells.
XX
SQ   Sequence 32 BP; 6 A; 12 C; 7 G; 7 T; 0 other;


  Query Match             8.4%;  Score 20;  DB 21;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0.52;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      65 cagggcagaggcgctaagcc 84
           ||||||||||||||||||||
Db      32 CAGGGCAGAGGCGCTAAGCC 13


RESULT  20
AAF58636/c
```

```
ID   AAF58636 standard; DNA; 32 BP.
XX
AC   AAF58636;
XX
DT   27-APR-2001  (first entry)
XX
DE   Human NY-ESO-1 PCR primer #2.
XX
KW   Human; NY ESO 1; HLA; human leukocyte antigen; CTL; cytotoxic T cell;
KW   HLA-A2; HLA-DR53; melanoma; adenocarcinoma; bladder carcinoma;
KW   non-small cell lung carcinoma; tumour status determination; PCR primer;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO200107917-A1.
XX
PD   01-FEB-2001.
XX
PF   14-JUL-2000; 2000WO-US19220.
XX
PR   23-JUL-1999;   99US-0359503.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
PA   (SLOK ) SLOAN KETTERING INST CANCER RES.
PA   (CORR ) CORNELL RES FOUND INC.
XX
PI   Jager E,  Stockert E,  Old LJ,  Knuth A,  Chen Y,  Scanlan M;
XX
DR   WPI; 2001-182822/18.
XX
PT   Method useful for determining the status (e.g. progression, regression
PT   or stability) of the disease) of a cancerous condition, involves
PT   determining the levels of NY-ESO-1 specific antibodies in a sample
PT   taken from a patient -
XX
PS   Example 6; Page 14; 50pp; English.
XX
CC   The present sequence was used to amplify a segment of human NY ESO 1
CC   cDNA in an example illustrating a method for determining the status of a
CC   cancerous condition in a patient with a tumour that expresses NY ESO-1.
CC   The method comprises assaying a sample taken from the patient for
CC   antibodies that specifically bind to the NY ESO 1 and comparing the
CC   value obtained to a prior value obtained from assay of a prior sample
CC   taken from the patient. Any difference between the values is indicative
CC   of a change in status of the cancerous condition. The method is useful
CC   for determining whether a cancerous condition is progressing, regressing
CC   or remaining stable, in particular in patients receiving treatment for a
CC   melanoma, adenocarcinoma, non-small cell lung carcinoma or bladder
CC   carcinoma.
XX
SQ   Sequence 32 BP; 6 A; 12 C; 7 G; 7 T; 0 other;


  Query Match             8.4%;  Score 20;  DB 22;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0.52;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      65 caqqqcaqaqqcqctaagcc 84
           ||||||||||||||||||||
Db      32 CAGGGCAGAGGCGCTAAGCC 13


RESULT  21
AAV50351/c
ID   AAV50351 standard; cDNA; 19 BP.
XX
AC   AAV50351;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Human LAGE-1 PCR primer BLE56.
XX
KW   Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour;
KW   PCR primer; ss.
XX
OS   Synthetic.
OS   Homo sapiens.
XX
PN   WO9832855-A1.
XX
PD   30-JUL-1998.
XX
PF   27-JAN-1998;   98WO-US01445.
XX
PR   27-JAN-1997;   97US-0791495.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Boon-Falleur T,  De Smet C,  Godelaine D,  Lethe B;
PI   Lucas S;
XX
DR   WPI; 1998-427651/36.
XX
PT   New isolated LAGE 1 tumour associated nucleic acids  used to
PT   develop products for the diagnosis and treatment of LAGE 1
PT   associated disorders, particularly tumours
XX
PS   Example 1; Page 58; 73pp; English.
XX
CC   The present sequence represents a PCR primer for LAGE 1 tumour
CC   associated protein (TAP). The present invention also describes: (1) a
CC   method for treating a subject with a disorder characterised by
CC   expression of a LAGE-1 nucleic acid molecule or an expressed prot.
CC   comprising administering to the subject autologous cytolytic T cells
CC   ameliorate the disorder, where the cytolytic T cells are specific for
CC   complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic
CC   fragment; (2) a method for treating a subject with a disorder
CC   characterised by expression of a LAGE-1 nucleic acid molecule or an
CC   expression product, comprising administering a LAGE 1 TAP or a
CC   immunogenic fragment to ameliorate the disorder; and (3) a method for
CC   selectively enriching a population of T cells with cytolytic T cells
CC   specific for a LAGE 1 TAP comprising contacting an isolated populatio
CC   of T cells with an agent presenting a complex of a LAGE TAP or an
CC   immunogenic fragment and a HLA presenting molecule to selectively
CC   enrich the isolated population of T cells with the cytolytic T cells.
CC   The methods and products from the present invention can be used for th
CC   diagnosis and treatment of LAGE 1 associated disorders, particularly
CC   tumours.
XX
SQ   Sequence 19 BP; 6 A; 5 C; 4 G; 2 T; 0 other;


  Query Match             8.0%;  Score 19;  DB 19;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 1.7;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 ttccctgttgatgtgtcate 24
           |||||||||||||||||||
Db      19 TTCCCTGTTGATGTGGCATC 1


RESULT  22
AAV50353/c
ID   AAV50353 standard; cDNA; 19 BP.
XX
AC   AAV50353;
XX
DT   27-OCT-1998  (first entry)
XX
DE   Human LAGE-1 PCR primer BLE71.
XX
KW   Human; LAGE-1; tumour associated protein; LL-1; diagnosis; tumour;
KW   PCR primer; ss.
XX
OS   Synthetic.
```

OS Homo sapiens.
XX
PN WO9832855 A1.
XX
PD 30-JUL-1998.
XX
PF 27-JAN-1998; 98WO-US001445.
XX
PR 27-JAN-1997; 97US-079149S.
XX
PA (LUDW) LUDWIG INST CANCER RES.
XX
PI Boon Falleur T, De Smet C, Godelaine D, Lethe B;
PI Lucas S;
XX
DR WPI; 1998-427951/36.
XX
PT New isolated LAGE-1 tumour associated nucleic acids - used to
PT develop products for the diagnosis and treatment of LAGE-1
PT associated disorders, particularly tumours
XX
PS Example 4; Page 59; 74pp; English.
XX
CC The present sequence represents a PCR primer for LAGE-1 tumour
CC associated protein (TAP). The present invention also describes: (1) a
CC method for treating a subject with a disorder characterised by
CC expression of a LAGE-1 nucleic acid molecule or an expression product,
CC comprising administering to the subject autologous cytolytic T cells to
CC ameliorate the disorder, where the cytolytic T cells are specific for
CC complexes of an HLA molecule and a LAGE-1 TAP or an immunogenic
CC fragment; (2) a method for treating a subject with a disorder
CC characterised by expression of a LAGE-1 nucleic acid molecule or an
CC expression product, comprising administering a LAGE-1 TAP or an
CC immunogenic fragment to ameliorate the disorder; and (4) a method for
CC selectively enriching a population of T cells with cytolytic T cells
CC specific for a LAGE-1 TAP comprising contacting an isolated population
CC of T cells with an agent presenting a complex of a LAGE TAP or an
CC immunogenic fragment and a HLA presenting molecule to selectively
CC enrich the isolated population of T cells with the cytolytic T cells.
CC The methods and products from the present invention can be used for the
CC diagnosis and treatment of LAGE-1 associated disorders, particularly
CC tumours.
XX
SQ Sequence 19 BP; 2 A; 6 C; 7 G; 4 T; 0 other;

Query Match 8.0%; Score 19; DB 19; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 tccccagccacgactgccccag 150
||||||||||||||||||||
Db 19 TCCCAGCACGAGTGGCCAG 1

RESULT 23
AAI79634
ID AAI79634 standard; DNA; 1898 BP.
XX
AC AAI79634;
XX
DT 15-OCT-1997 (first entry)
XX
DE DNA encoding human ubiquitous nuclear receptor polypeptide.
XX
KW Ubiquitous nuclear receptor polypeptide; DNA binding domain;
KW therapy; drug design; diagnosis; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 71..1453
FT /*tag= a
XX
PN US5639616-A.
XX
PD 17-JUN-1997.
XX
PF 10-NOV-1993; 93US-0152003.
XX
PR 18-NOV-1994; 94US-0342411.
PR 10-NOV-1993; 93US-0152003.
XX
PA (ARCH-) ARCH DEV CORP.
XX
PI Liao S, Sood C;
XX
DR WPI; 1997-332343/30.
DR P-PSDB; AAW25034.
XX
PT DNA encoding ubiquitous nuclear receptor polypeptide - is
PT producing recombinant polypeptide(s) and detecting DNA
XX
PS Claim 1; Column 67 2@; 67pp; English.
XX
CC AAI79634 encodes a human ubiquitous nuclear receptor polypeptide (UNR).
CC The UR is useful in assays designed to select substances which
CC interact with the UR which may potentially be of use therapeutically.
CC UR is also used in diagnosis and drug design.
XX
SQ Sequence 1898 BP; 436 A; 599 C; 541 G; 322 T; 0 other;

Query Match 8.0%; Score 19; DB 18; Length 1898;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 cagcctgacgcccctttct 103
|||||||||||||||||||
Db 125 cagcctgacgcccctttct 143

RESULT 24
AAC53480/c
ID AAC53480 standard; DNA; 1444 BP.
XX
AC AAC53480;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 7442.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.

PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
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DT 06-APR-1999 (first entry)
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DE Genomic DNA sequence of Brassica FadZ U gene.
XX
KW Fatty acid desaturase; FAD; Brassicaceae; Helianthus; mutation;
KW fatty acid; oleic acid; linoleic acid; FadZ gene; ss.
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OS Brassica napus.
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PF 11-JUN-1998; 98WO-US12332.
XX
PR 12-JUN-1997; 97US-0874109.
XX
PA (CARG-) CARGILL INC.
XX
PI DeBonte ER, Loh WH, Shorrosh BS, Zhegong F;
XX
DR WPI; 1999-059929/05.
DR P-PSDB; AAW94056.
XX
PT New isolated mutant fatty acid desaturase genes - obtained by
PT mutation of Brassicaceae or Helianthus plants, used to producing
PT plants or seeds having altered fatty acid compositions
XX
PS Claim 88; Pages 86-87; 116pp; English.
XX
CC The invention relates to fatty acid desaturases (FADs) in Brassicaceae
CC or Helianthus, where the FAD genes comprise at least one substitution in
CC their sequences. The mutation is in a region encoding the HD-Xaa-Xaa-Xaa
CC His motif of the delta 12 or delta 15 fatty acid desaturases. The
CC invention also provides methods for producing the FAD mutant nucleic acid
CC gene products. The products can be used for producing plants and seeds
CC which have altered fatty acid compositions, esp. an elevated oleic acid
CC content, a decreased, stabilised linoleic acid content, both elevated
CC oleic acid and decreased, stabilised linoleic acid content or a
CC decreased, stabilised level of alpha-linolenic acid and increased level
CC of linoleic acid. The plants may be e.g. soybean, rapeseed, sunflower,
CC safflower, castor bean or corn. The present sequence represents the
CC genomic DNA sequence of the Brassica wild type FadZ U gene.
XX
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Query Match 7.6%; Score 18; DB 26; Length 2168;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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GenCore version 4.5
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OM nucleic - nucleic search, using sw model

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ALIGNMENTS

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; Patent No. 5811519
; GENERAL INFORMATION:
; APPLICANT: Leth, Bernard
; APPLICANT: [illegible], Sophie
; APPLICANT: De Smet, Charles
; APPLICANT: Godelaine, Danielle
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: [illegible] NUMBER OF SPECIFIC GENES
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
; STREET: 600 Atlantic Avenue
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/791,495
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Van Amsterdam, John R.
; REGISTRATION NUMBER: 40,212
; REFERENCE/DOCKET NUMBER: 13401/7005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617 720 3500
; TELEFAX: 617 720 2441
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1002 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:

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;       LOCATION:  65..697
US-08-791-495-4


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;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL-1 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  Patentin Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John P.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  [illegible]
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
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;    ANTI-SENSE:  NO
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;       LOCATION:  53..595
US-08-791-495-6


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;  GENERAL INFORMATION:
;    APPLICANT:  Yao Tseng Chen, Scanlan, Matthew, Gure, Ali,
;    APPLICANT:  Old, Lloyd
;    TITLE OF INVENTION:  ISOLATED NUCLEIC ACID MOLECULE ENCODING
;    TITLE OF INVENTION:  AN ESOPHAGEAL CANCER ASSOCIATED ANTIGEN, ITS ANTIGEN ITSELF
;    TITLE OF INVENTION:  AND USES THEREOF
;    NUMBER OF SEQUENCES:  1
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 1.44 MB storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  Wordperfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/725,182C
;      FILING DATE:  03-October-1996
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 5804381man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  752 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-08-725-182C-1


  Query Match             71.4%;  Score 170;  DB 1;  Length 752;
  Best Local Similarity   99.5%;  Pred. No. 2.6e-80;
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Matches 220; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cagcttttccctgttgatgtgggatcacgcagtgcttttctgcccgtgttttgggctcagcct 60
Db 516 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTGGGCTCAGCCT 575

Qy 61 ccctcagggcagagggcgctaaggccagccctggcgccgccttgctaggtcatgcctcctcct 120
Db 576 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCCTGGCGCCGCCTTGCTAGGTCATGCCTCCTCCC 635

Qy 121 ctagggaatcgtcccagcacgaatgcgccagttcattgtgcgggcctgattgtttgtcgct 180
Db 636 CTAGGGAATCGTCCCAGCACGAGTGCGCCAGTTCATTGTGCGGGGCCTGATTGTTTGTCGCT 695

Qy 181 qqaqqaqqacqqcttacatgtttgtttctgtaaaaataaa 221
Db 696 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 736

RESULT 4
US-09-014-150-1
; Sequence 1, Application US/09014150
; Patent No. 6069233
; GENERAL INFORMATION:
; APPLICANT: Yao-Tseng Chen, Scanlan, Matthew, Gure, Ali,
; APPLICANT: Old, Lloyd
; TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING
; TITLE OF INVENTION: AN ESOPHAGEAL CANCER ASSOCIATED ANTIGEN, THE ANTIGEN ITSELF,
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 1
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lynch
; STREET: 805 Third Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10022
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.5 inch, 1.44 MB storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/014,150
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/725,128
; FILING DATE: 04-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 606928man D
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 688-9200
; TELEFAX: (212) 838-3884
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-014-150-1

Query Match 71.4%; Score 170; DB 3; Length 752;
Best Local Similarity 99.5%; Pred. No. 2.6e-80;
Matches 220; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cagcttttccctgttgatgtgggatcacgcagtgcttttctgcccgtgttttgggctcagcct 60
Db 516 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTGGGCTCAGCCT 575

Qy 61 ccctcagggcagagggcgctaaggccagccctggcgccgccttgctaggtcatgcctcctcct 120
Db 576 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCCTGGCGCCGCCTTGCTAGGTCATGCCTCCTCCC 635

Qy 121 ctagggaatcgtcccagcacgaatgcgccagttcattgtgcgggcctgattgtttgtcgct 180
Db 636 CTAGGGAATCGTCCCAGCACGAGTGCGCCAGTTCATTGTGCGGGGCCTGATTGTTTGTCGCT 695

Qy 181 qqaqqaqqacqqcttacatgtttgtttctgtaaaaataaa 221
Db 696 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 736

RESULT 5
US-09-359-503-1
; Sequence 1, Application US/09359503
; Patent No. 6251603
; GENERAL INFORMATION:
; APPLICANT: Jager, Elke; Stockert, Elisabeth; Old, Lloyd J.
; APPLICANT: Knuth, Alexander
; TITLE OF INVENTION: Method for Determining Status of A
; TITLE OF INVENTION: Cancerous Condition By Determining Activity
; TITLE OF INVENTION: a Patient Sample
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fulbright & Jaworski, L.L.P.
; STREET: 666 Fifth Avenue
; CITY: New York City
; STATE: New York
; COUNTRY: USA
; ZIP: 10103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
; COMPUTER: IBM
; OPERATING SYSTEM: PC-DOS
; SOFTWARE: WordPerfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/359,503
; FILING DATE: July 23, 1999
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/165,546
; FILING DATE: October 2, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/062,422
; FILING DATE: April 17, 1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/937,259
; FILING DATE: September 15, 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/752,182
; FILING DATE: 05-October-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Hanson, No. 625160man D
; REGISTRATION NUMBER: 30,946
; REFERENCE/DOCKET NUMBER: LUD 5466.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 318-3000
; TELEFAX: (212) 752-5958
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 752 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-09-359-503-1

Query Match 71.4%; Score 170; DB 4; Length 752;
Best Local Similarity 99.5%; Pred. No. 2.6e-80;
Matches 220; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 cagcttttccctgttgatgtgggatcacgcagtgcttttctgcccgtgttttgggctcagcct 60

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| 61
Db    516 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGCCC 575

Qy     61 ccctcaqqqcaqaqqcqctaaqcccaqcctgqcqcccctttcctaqqtcatqcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    576 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 635

Qy    121 ctaqqaatqqtcccaqcacqaqtqqccaqttcattqtqqqqqcctqattqtttqtcqct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    636 CTAGGCAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCCTGATTGTTTGTCGCT 695

Qy    181 qqaqqaqqacqqcttacatqtttqtttctqtaqaaaataaa 221
              |||||||||||||||||||||||||||||||||||||||||
Db    696 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 736


RESULT   6
US-09-062-422-1
; Sequence 1, Application US/09062422
; Patent No. 6252052
;  GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander;
;    APPLICANT:  Old, Lloyd J.
;    TITLE OF INVENTION:  ANTIBODIES WHICH BIND TO NY-ESO-1
;    TITLE OF INVENTION:  CANCER ASSOCIATED PROTEINS, USES THEREOF, TRUNCATED
;    TITLE OF INVENTION:  FORMS OF NY-ESO-1, AND HLA BINDING PEPTIDES DERIVED
;    TITLE OF INVENTION:  THEREFROM
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Felfe & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/062,422
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/937,263
;      FILING DATE:  September 15, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 08/752,182
;      FILING DATE:  03-October-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6252052man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688 9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  752 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
US-09-062-422-1


  Query Match             71.4%;  Score 170;  DB 4;  Length 752;
  Best Local Similarity   99.5%;  Pred. No. 2.6e-80;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 caqctttccctgttgatgtggatcacgcagtgctttctgcccgtgttttttggctcagccct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
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Db    516 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGCCC 575

Qy     61 ccctcaqqqcaqaqqcqctaaqcccaqcctqqcqcccctttcctaqqtcatqcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    576 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 635

Qy    121 ctaqqaatqqtcccaqcacqaqtqqccaqttcattqtqqqqqcctqattqtttqtcqct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    636 CTAGGCAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCCTGATTGTTTGTCGCT 695

Qy    181 qqaqqaqqacqqcttacatqtttqtttctqtaqaaaataaa 221
              |||||||||||||||||||||||||||||||||||||||||
Db    696 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 736


RESULT   7
US-09-396-184-1
; Sequence 1, Application US/09396184
; Patent No. 6255470
;   GENERAL INFORMATION:
;        APPLICANT: Yao Tseng Chen, Scanlan, Matthew, Gure, A.;
;                   Old, Lloyd
;        TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE ENCODING
;                            AN ESOPHAGEAL CANCER ASSOCIATED ANTIGEN, AND ANTIBODIES
;                            AND USES THEREOF
;        NUMBER OF SEQUENCES: 1
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Felfe & Lynch
;             STREET: 805 Third Avenue
;             CITY: New York City
;             STATE: New York
;             COUNTRY: USA
;             ZIP: 10022
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Diskette, 3.5 inch, 1.44 MB storage
;             COMPUTER: IBM
;             OPERATING SYSTEM: PC-DOS
;             SOFTWARE: WordPerfect
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/396,184
;             FILING DATE: 14-Sep-1999
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 09/014,150
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Hanson, No. 6255470man D.
;             REGISTRATION NUMBER: 30,946
;             REFERENCE/DOCKET NUMBER: LUD 5466
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (212) 688-9200
;             TELEFAX: (212) 838-3884
;   INFORMATION FOR SEQ ID NO: 1:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 752 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-396-184-1


  Query Match             71.4%;  Score 170;  DB 4;  Length 752;
  Best Local Similarity   99.5%;  Pred. No. 2.6e-80;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy       1 caqctttccctgttgatgtggatcacgcagtgctttctgcccgtgttttttggctcagccct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db    516 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGCCC 575

Qy     61 ccctcaqqqcaqaqqcqctaaqcccaqcctqqcqcccctttcctaqqtcatqcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    576 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 635
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Qy        121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        636 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCGCT 695

Qy        181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
              |||||||||||||||||||||||||||||||||||||||||
Db        696 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 736


RESULT  8
US-08-791-495-8
; Sequence 8, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL 2 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7060
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  755 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  51..593
US-08-791-495-8

  Query Match             71.4%;  Score 170;  DB 1;  Length 755;
  Best Local Similarity   99.5%;  Pred. No. 2.6e-80;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        513 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGCCT 572

Qy         61 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        573 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 632
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Qy        121 ctagggaatggtcccagcacgagtggccagttcattgtggggcct[illegible]
              ||||||||||||||||||||||||||||||||||||||||||  |||||||||||||
Db        633 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTTATTGTTTGTCGCT 692

Qy        181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
              |||||||||||||||||||||||||||||||||||||||||
Db        693 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 733


RESULT  9
US-08-791-495-1
; Sequence 1, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;    APPLICANT:  Leth , Bernard
;    APPLICANT:  Lucas, Sophie
;    APPLICANT:  De Smet, Charles
;    APPLICANT:  Godelaine, Daniele
;    APPLICANT:  Boon-Falleur, Thierry
;    TITLE OF INVENTION:  LL 2 TUMOR SPECIFIC GENES
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;      STREET:  600 Atlantic Avenue
;      CITY:  Boston
;      STATE:  MA
;      COUNTRY:  USA
;      ZIP:  02210
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/791,495
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Van Amsterdam, John R.
;      REGISTRATION NUMBER:  40,212
;      REFERENCE/DOCKET NUMBER:  L0461/7060
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-720-3500
;      TELEFAX:  617-720-2441
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  217 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
;    HYPOTHETICAL:  NO
;    ANTI-SENSE:  NO
;    FRAGMENT TYPE:  internal
;    ORIGINAL SOURCE:
;      ORGANISM:  Homo sapiens
US-08-791-495-1

  Query Match             10.1%;  Score 24;  DB 1;  Length 217;
  Best Local Similarity   100.0%;  Pred. No. 0.0011;
  Matches   24;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 cagctttccctgttgatgtggatc 24
              ||||||||||||||||||||||||
Db        194 CAGCTTTCCCTGTTGATGTGGATC 217


RESULT  10
US-09-105-907-10/c
; Sequence 10, Application US/09105907A
; Patent No. 6140050
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; GENERAL INFORMATION:
;  APPLICANT: Sahin, Ugur
;  APPLICANT: Tureci, Ozlem
;  APPLICANT: Chen, Yao-Tseng
;  APPLICANT: Old, Lloyd
;  APPLICANT: Pfreundschuh, Michael
;  TITLE OF INVENTION: Methods For Determining Breast Cancer And Melanoma By Assaying
;  TITLE OF INVENTION: For A Plurality of Antigens Associated Therewith
;  FILE REFERENCE: LUD 5544
;  CURRENT APPLICATION NUMBER: US/09/105,907A
;  CURRENT FILING DATE: 1998-06-26
;  NUMBER OF SEQ ID NOS: 18
; SEQ ID NO 10
;   LENGTH: 32
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
US-09-105-907-10


  Query Match              8.4%;  Score 20;  DB 4;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      65 cagggcagaggcgctaagcc 84
           ||||||||||||||||||||
Db      32 CAGGGCAGAGGCGCTAAGCC 13


RESULT  11
US-09-459-503-3/c
; Sequence 3, Application US/09459503
; Patent No. 6251602
;  GENERAL INFORMATION:
;    APPLICANT:  Jager, Elke; Stockert, Elisabeth; Old, Lloyd J;
;    APPLICANT:  Knuth, alexander
;    TITLE OF INVENTION:  Method for Determining Status of A
;    TITLE OF INVENTION:  Cancerous Condition By Determining Antibodies              to NY
;    TITLE OF INVENTION:  a Patient Sample
;    NUMBER OF SEQUENCES:  14
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Fulbright & Jaworski, L.L.P.
;      STREET:  666 Fifth Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10103
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/459,503
;      FILING DATE:  July 23, 1999
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/165,546
;      FILING DATE:  October 2, 1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  09/062,422
;      FILING DATE:  April 17, 1998
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/937,263
;      FILING DATE:  September 15, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/752,182
;      FILING DATE:  03-October-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6251603man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 318-3000
;      TELEFAX:  (212) 752-5958
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-459-503-3


  Query Match              8.4%;  Score 20;  DB 4;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      65 cagggcagaggcgctaagcc 84
           ||||||||||||||||||||
Db      32 CAGGGCAGAGGCGCTAAGCC 13


RESULT  12
US-09-062-422-3/c
; Sequence 3, Application US/09062422
; Patent No. 6252052
;  GENERAL INFORMATION:
;    APPLICANT:  Stockert, Elisabeth; Jager, Elke;
;    APPLICANT:  Chen, Yao-Tseng; Scanlan, Matthew; Knuth, Alexander
;    APPLICANT:  Old, Lloyd J.
;    TITLE OF INVENTION:  ANTIBODIES WHICH BIND TO NY-ESO-1
;    TITLE OF INVENTION:  CANCER ASSOCIATED PROTEINS, USES THEREOF AND DNA ENC
;    TITLE OF INVENTION:  FORMS OF NY ESO 1, AND HLA BINDING PEPTIDES DERIVED
;    TITLE OF INVENTION:  THEREFROM
;    NUMBER OF SEQUENCES:  7
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Foley & Lynch
;      STREET:  805 Third Avenue
;      CITY:  New York City
;      STATE:  New York
;      COUNTRY:  USA
;      ZIP:  10022
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inch, 144 kb storage
;      COMPUTER:  IBM
;      OPERATING SYSTEM:  PC-DOS
;      SOFTWARE:  WordPerfect
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/062,422
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/937,263
;      FILING DATE:  September 15, 1997
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US 09/752,182
;      FILING DATE:  03-October-1996
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Hanson, No. 6252052man D.
;      REGISTRATION NUMBER:  30,946
;      REFERENCE/DOCKET NUMBER:  LUD 5466.3
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (212) 688-9200
;      TELEFAX:  (212) 838-3884
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  32 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-09-062-422-3


  Query Match              8.4%;  Score 20;  DB 4;  Length 32;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
```

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  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      65 caggccagaggcgctaaagcc 84
           |||||||||||||||||||||
Db      42 CAGGCCAGAGGCGCTAAAGCC 13


RESULT  13
US-08-791-495-3/c
; Sequence 3, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;     APPLICANT:  Leth , Bernard
;     APPLICANT:  Lucas, Sophie
;     APPLICANT:  De Smet, Charles
;     APPLICANT:  Godefaine, Daniele
;     APPLICANT:  Boon-Falleur, Thierry
;     TITLE OF INVENTION:  IL 13 TUMOR SPECIFIC GENES
;     NUMBER OF SEQUENCES:  14
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;       STREET:  600 Atlantic Avenue
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/791,495
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Van Amsterdam, John R.
;       REGISTRATION NUMBER:  40,212
;       REFERENCE/DOCKET NUMBER:  1041/7005
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617 720 4500
;       TELEFAX:  617 720-2441
;   INFORMATION FOR SEQ ID NO:  4:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  19 nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  YES
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
US-08-791-495-4


  Query Match             8.0%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.43;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       6 tttccctattatatgaatc 24
           |||||||||||||||||||
Db      19 TTCCCTGTTGTATGTGGATC 1


RESULT  14
US-08-791-495-11/c
; Sequence 11, Application US/08791495
; Patent No. 5811519
;  GENERAL INFORMATION:
;     APPLICANT:  Leth , Bernard
;     APPLICANT:  Lucas, Sophie
;     APPLICANT:  De Smet, Charles
;     APPLICANT:  Godefaine, Daniele
;     APPLICANT:  Boon-Falleur, Thierry
;     TITLE OF INVENTION:  IL 13 TUMOR SPECIFIC GENES
;     NUMBER OF SEQUENCES:  14
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Wolf, Greenfield & Sacks, P.C.
;       STREET:  600 Atlantic Avenue
;       CITY:  Boston
;       STATE:  MA
;       COUNTRY:  USA
;       ZIP:  02210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/791,495
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Van Amsterdam, John R.
;       REGISTRATION NUMBER:  40,212
;       REFERENCE/DOCKET NUMBER:  1041/7005
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  617-720-4500
;       TELEFAX:  617 720 2441
;   INFORMATION FOR SEQ ID NO:  11:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  19 nucleotides
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
;     HYPOTHETICAL:  NO
;     ANTI-SENSE:  YES
;     ORIGINAL SOURCE:
;       ORGANISM:  Homo sapiens
US-08-791-495-11


  Query Match             8.0%;  Score 19;  DB 1;  Length 19;
  Best Local Similarity   100.0%;  Pred. No. 0.43;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     132 tccaagcagaagatgcaac 150
           |||||||||||||||||||
Db      19 TCCCAGCAGGAGTGGCAAC 1


RESULT  15
US-09-183-951-22/c
; Sequence 22, Application US/09183951C
; Patent No. 6210886
; GENERAL INFORMATION:
;  APPLICANT: Van Baren, Nicolas
;  APPLICANT: Brasseur, Francis
;  APPLICANT: Boon Falleur, Thierry
;  TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETECTING
;  TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
;  FILE REFERENCE: LUC 5527.1 JEL/ES
;  CURRENT APPLICATION NUMBER: US/09/183,951C
;  CURRENT FILING DATE: 2000-02-28
;  EARLIER APPLICATION NUMBER: US 09/018,422
;  EARLIER FILING DATE: 1998   02   04
;  NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 22
;   LENGTH: 19
;   TYPE: DNA
;   ORGANISM: Artificial sequence
;   FEATURE:
;   NAME/KEY: PCR primer
;   OTHER INFORMATION: Synthesized by oligonucleotide synthesis machine
```

US-09-183-931-22

Query Match 8.0%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 tcccaqcacqaqtqqccaq 150
||||||||||||||||||||
Db 19 TCCCAGCACGAGTGGCCAG 1

RESULT 16
US-09-183-931-24/c
; Sequence 24, Application US/09183931C
; Patent No. 6210886
; GENERAL INFORMATION:
; APPLICANT: Van Baren, Nicolas
; APPLICANT: Brasseur, Francis
; APPLICANT: Boon-Falleur, Thierry
; TITLE OF INVENTION: METHOD FOR DIAGNOSING LEUKEMIA BY DETERMINING
; TITLE OF INVENTION: TUMOR REJECTION ANTIGEN PRECURSORS
; FILE REFERENCE: LUD 6527.1 'FL/ES
; CURRENT APPLICATION NUMBER: US/09/183,931C
; CURRENT FILING DATE: 2000-02-28
; EARLIER APPLICATION NUMBER: US 09/018,422
; EARLIER FILING DATE: 1998 - 02 - 04
; NUMBER OF SEQ ID NOS: 44
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PCR primer
; OTHER INFORMATION: Synthesized by oligonucleotide synthesis machine
US-09-183-931-24

Query Match 8.0%; Score 19; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 132 tcccaqcacqaqtqqccaq 150
||||||||||||||||||||
Db 19 TCCCAGCACGAGTGGCCAG 1

RESULT 17
US-08-342-411A-1
; Sequence 1, Application US/08342411A
; Patent No. 5639616
; GENERAL INFORMATION:
; APPLICANT: LIAO, Shutsung
; APPLICANT: SONG, Ching
; TITLE OF INVENTION: UBIQUITOUS NUCLEAR RECEPTOR
; TITLE OF INVENTION: COMPOSITIONS AND METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/342,411A
; FILING DATE: 18-NOV-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: KITCHELL, BARBARA S.
; REGISTRATION NUMBER: 33,929
; REFERENCE/DOCKET NUMBER: ARCD154
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (714) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1898 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 71..1450
US-08-342-411A-1

Query Match 8.0%; Score 19; DB 1; Length 1898;
Best Local Similarity 100.0%; Pred. No. 0.47;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 85 cagcctggccgccccttcct 103
||||||||||||||||||||
Db 125 CAGCCTGGCCGCCCCTTCCT 143

RESULT 18
US-08-684-687-2/c
; Sequence 3, Application US/08684687
; Patent No. 5830451
; GENERAL INFORMATION:
; APPLICANT: KIEFF, ELLIOTT D.
; APPLICANT: DEVERGNE, ODILE
; TITLE OF INVENTION: A NOVEL HAEMATOPOIETIC CYTOKINE AND USES
; TITLE OF INVENTION: THEREFOR
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WOLF, GREENFIELD & SACKS, P.C.
; STREET: 600 ATLANTIC AVENUE
; CITY: BOSTON
; STATE: MA
; COUNTRY: USA
; ZIP: 02210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/684,687
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/005,092
; FILING DATE: 11-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: GATES, EDWARD R.
; REGISTRATION NUMBER: 41,616
; REFERENCE/DOCKET NUMBER: 8'[illegible]/7051
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-720-3500
; TELEFAX: 617-720-2441
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1316 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO

; ANTI SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: HOMO SAPIENS
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 102..863
US-08-684-667-3

Query Match 7.1%; Score 17; DB 2; Length 1416;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 192 gcttacatgtttgttc 208
||||||||||||||||
Db 1165 GCTTACATGTTTGTTC 1149

RESULT 19
US-08-265-087-3/c
; Sequence 3, Application US/08265087
; Patent No. 5571515
; GENERAL INFORMATION:
; APPLICANT: Scott, Phillip
; APPLICANT: Trinchieri, Giorgio
; TITLE OF INVENTION: Compositions and Methods for Use of
; TITLE OF INVENTION: IL-12 as an Adjuvant
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Center, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/265,087
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/229,282
; FILING DATE: 18-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WS1S1AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1364 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 101..859
US-08-265-087-3

Query Match 7.1%; Score 17; DB 1; Length 1364;
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 192 gcttacatgtttgttc 208
||||||||||||||||
Db 1165 GCTTACATGTTTGTTC 1149

RESULT 20
US-08-621-493-3
; Sequence 3, Application US/08621493
; Patent No. 5723127
; GENERAL INFORMATION:
; APPLICANT: Scott, Phillip
; APPLICANT: Trinchieri, Giorgio
; TITLE OF INVENTION: Compositions and Methods [illegible]
; TITLE OF INVENTION: IL-12 as an Adjuvant
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Center, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/621,493
; FILING DATE: 25-MAR-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/265,087
; FILING DATE: 17-JUN-1994
; APPLICATION NUMBER: US 08/229,282
; FILING DATE: 18-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: WS1S1AUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-540-9206
; TELEFAX: 215-540-5818
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1364 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: unknown
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 101..859
US-08-621-493-3

Query Match 7.1%; Score 17; DB 1; Length [illegible];
Best Local Similarity 100.0%; Pred. No. 5.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 192 gcttacatgtttgttc 208
||||||||||||||||
Db 1165 GCTTACATGTTTGTTC 1149

RESULT 21
US-08-965-688-3/c
; Sequence 3, Application US/08965688
; Patent No. 5976509
; GENERAL INFORMATION:
; APPLICANT: Scott, Phillip
; APPLICANT: Trinchieri, Giorgio
; TITLE OF INVENTION: Compositions and Methods for Use [illegible]
; TITLE OF INVENTION: IL-12 as an Adjuvant
; NUMBER OF SEQUENCES: 4

```
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  Howson and Howson
;      STREET:  Spring House Corporate Center, PO Box 457
;      CITY:  Spring House
;      STATE:  Pennsylvania
;      COUNTRY:  USA
;      ZIP:  19477
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/965,688
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/621,493
;      FILING DATE:  25-MAR-1996
;      APPLICATION NUMBER:  08/265,087
;      FILING DATE:  17-JUN-1994
;      APPLICATION NUMBER:  US 08/229,282
;      FILING DATE:  18-APR-1994
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Bak, Mary E.
;      REGISTRATION NUMBER:  31,215
;      REFERENCE/DOCKET NUMBER:  WST51AUSA
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  215-540-9206
;      TELEFAX:  215-540-5818
;  INFORMATION FOR SEQ ID NO:  3:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  1364 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  unknown
;    MOLECULE TYPE:  cDNA
;    FEATURE:
;      NAME/KEY:  CDS
;      LOCATION:  101..859
US-08-965-688-3


  Query Match              7.1%;  Score 17;  DB 2;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 5.3;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     192 gcttacatgtttgtttc 208
           |||||||||||||||||
Db    1165 GCTTACATGTTTGTTTC 1149


RESULT  22
US-09-260-173-3/c
; Sequence 3, Application US/09260173
; Patent No. 6168923
;   GENERAL INFORMATION:
;        APPLICANT: Scott, Phillip
;                   Trinchieri, Giorgio
;        TITLE OF INVENTION: Compositions and Methods for Use of
;                            IL-12 as an Adjuvant
;        NUMBER OF SEQUENCES: 4
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: Howson and Howson
;             STREET: Spring House Corporate Center, PO Box 457
;             CITY: Spring House
;             STATE: Pennsylvania
;             COUNTRY: USA
;             ZIP: 19477
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.?
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/260,173
;             FILING DATE: 01-Mar-1999
;             CLASSIFICATION: <Unknown>
;                             17-JUN-1994
;                             18-APR-1994
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/965,688
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/265,087
;             FILING DATE: 17-JUN-1994
;             APPLICATION NUMBER: US 08/229,282
;             FILING DATE: 18 APR 1994
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Bak, Mary E.
;             REGISTRATION NUMBER: 31,215
;             REFERENCE/DOCKET NUMBER: WST51AUSA
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: 215 540 9206
;             TELEFAX: 215-540-5818
;   INFORMATION FOR SEQ ID NO: 3:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 1364 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: unknown
;        MOLECULE TYPE: cDNA
;        FEATURE:
;             NAME/KEY:  CDS
;             LOCATION:  101..859
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-260-173-3


  Query Match              7.1%;  Score 17;  DB 4;  Length 1364;
  Best Local Similarity   100.0%;  Pred. No. 5.3;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     192 gcttacatgtttgtttc 208
           |||||||||||||||||
Db    1165 GCTTACATGTTTGTTTC 1149


RESULT  23
US-08-649-619B-2
; Sequence 2, Application US/08649619B
; Patent No. 5871916
;  GENERAL INFORMATION:
;    APPLICANT:  NAKAMURA, YUSUKE
;    APPLICANT:  SAITO, HIROKO
;    TITLE OF INVENTION:  HUMAN PROTEIN AND DNA
;    TITLE OF INVENTION:  ENCODING THE SAME
;    NUMBER OF SEQUENCES:  11
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  FLYNN, THIEL, BOUTELL &
;      ADDRESSEE:  TANIS, P.C.
;      STREET:  2026 Rambling Road
;      CITY:  Kalamazoo
;      STATE:  Michigan
;      COUNTRY:  USA
;      ZIP:  49008-1699
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Diskette, 3.5 inches, 1.44 Mb
;      MEDIUM TYPE:  storage
;      COMPUTER:  IBM PC/AT Compatible
;      OPERATING SYSTEM:  MS-DOS 5.0
;      SOFTWARE:  WordPerfect 5.0
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/649,619B
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
```

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;       APPLICATION NUMBER:  JP6 226270
;       FILING DATE:  21 SEPT-1994
;       APPLICATION NUMBER:  PCT/JP95/01909
;       FILING DATE:  21 SEPT-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Terryence F. Chapman
;       REGISTRATION NUMBER:  32549
;       REFERENCE/DOCKET NUMBER:  Furuya Case 1343
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (616) 381-1156
;       TELEFAX:  (616) 381 5465
;   INFORMATION FOR SEQ ID NO:  2:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1688
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Homosapiens
US-08-649-6198-2

  Query Match             7.1%;  Score 17;  DB 2;  Length 1688;
  Best Local Similarity   100.0%;  Pred. No. 5.3;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      85 caqectqaqcgcccctlc 101
           |||||||||||||||||
Db     264 CAGCCTGGCGCGCCCTLC 279


RESULT  24
PCT US94 12884-3
; Sequence 3, Application PCT/US9412884
;  GENERAL INFORMATION:
;     APPLICANT:
;     TITLE OF INVENTION:  HBI-QUINONE NUCLEAR RECEPTOR COMPOSITIONS AND
;     TITLE OF INVENTION:  METHODS
;     NUMBER OF SEQUENCES:  48
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  Arnold, White & Durkee
;       STREET:  P.O. Box 4433
;       CITY:  Houston
;       STATE:  Texas
;       COUNTRY:  United States of America
;       ZIP:  77210
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS/AS400
;       SOFTWARE:  Patentin Release #1.0, Version
;       SOFTWARE:  #1.25
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  PCT/US94/12884
;       FILING DATE:  Concurrently Herewith
;       CLASSIFICATION:
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  US 08/152,054
;       FILING DATE:  10-NOV-1994
;       CLASSIFICATION:
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  BARBARA S. KITCHELL
;       REGISTRATION NUMBER:  33,928
;       REFERENCE/DOCKET NUMBER:  APC01541P
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (512) 418-3000
;       TELEFAX:  (713) 789-2679
;       TELEX:  79-0924
;   INFORMATION FOR SEQ ID NO:  3:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1813 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  single
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  DNA (genomic)
PCT US94-12884-3

  Query Match             7.1%;  Score 17;  DB 5;  Length 1813;
  Best Local Similarity   100.0%;  Pred. No. 5.3;
  Matches   17;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      85 caqectqaqcgcccctlc 101
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Db      40 CAGCCTGGCGCGCCCTLC 56


RESULT  25
US-08-649-6198-1
; Sequence 1, Application US/08649619B
; Patent No. 5871916
;  GENERAL INFORMATION:
;     APPLICANT:  NAKAMURA, YUSUKE
;     APPLICANT:  SAITO, HIROKO
;     TITLE OF INVENTION:  EGFR PROTEIN AND DNA
;     TITLE OF INVENTION:  ENCODING THE SAME
;     NUMBER OF SEQUENCES:  11
;     CORRESPONDENCE ADDRESS:
;       ADDRESSEE:  FLYNN, THIEL, BOUTELL &
;       ADDRESSEE:  TANIS, P.C.
;       STREET:  2026 Rambling Road
;       CITY:  Kalamazoo
;       STATE:  Michigan
;       COUNTRY:  USA
;       ZIP:  49008-1699
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Diskette, 3.5 inches, 1.44 MB
;       MEDIUM TYPE:  storage
;       COMPUTER:  IBM PC/XT/AT Compatible
;       OPERATING SYSTEM:  MS DOS 5.0
;       SOFTWARE:  WordPerfect 5.0
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/649,619B
;       FILING DATE:
;       CLASSIFICATION:  435
;     PRIOR APPLICATION DATA:
;       APPLICATION NUMBER:  JP6 226270
;       FILING DATE:  21-SEPT-1994
;       APPLICATION NUMBER:  PCT/JP95/01909
;       FILING DATE:  21-SEPT-1995
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  Terryence F. Chapman
;       REGISTRATION NUMBER:  32549
;       REFERENCE/DOCKET NUMBER:  Furuya Case 1343
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (616) 381 1156
;       TELEFAX:  (616) 381 5465
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  1979
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA to mRNA
;     ORIGINAL SOURCE:
;       ORGANISM:  Homosapiens
;     IMMEDIATE SOURCE:
;       LIBRARY:  Human mammary gland cDNA
;       LIBRARY:  library
;     FEATURE:
;       NAME/KEY:  CDS
;       LOCATION:  206..1791
;       IDENTIFICATION METHOD:  experimental examination
US-08-649-6198-1
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Query Match 7.1%; Score 17; DB 2; Length 1979;
Best Local Similarity 100.0%; Pred. No. 5.4;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db     263 CAGCCTGGCGCCCCTTC 279
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Search completed: October 9, 2001, 15:36:04
Job time: 2824 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 9, 2001, 14:02:40 ; Search time 1369.25 Seconds
(without alignments)
1643.074 Million cell updates/sec

Title: US-09-341-829A-4_COPY_756_993
Perfect score: 238
Sequence: 1 cagcttttccctgttgatgtg.....aaagctgagctacgattccg 238

Scoring table: OLIGO_NUC
Gapop 60.0 , Gapext 60.0

Searched: 10228115 seqs, 4726426750 residues

Word size : 0

Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

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253: em_qss_rod6:*
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256: qb_qss35:*
257: qb_qss36:*
258: qb_qss37:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result No.		Score	% Query Match	Length	DB	ID	Description
1		192	80.7	646	167	BE410697	BE410697 601300763
2	c	170	71.4	281	13	AA634317	AA634317 zu78c05.s
3	c	170	71.4	359	17	AI218223	AI218223 qh23a03.x
4		163	68.5	700	106	AL553954	AL553954 AL553954
5	c	110	46.2	629	106	AL553953	AL553953 AL553953
6	c	66	27.7	852	167	BE385880	BE385880 601275948
7		25	10.5	770	155	BG575764	BG575764 602597257
8	c	23	9.7	148	13	AA866133	AA866133 oh53d09.s
9		20	8.4	603	241	AZ312149	AZ312149 1M0027A23
10	c	19	8.0	261	124	BB056358	BB056358 BB056358
11	c	19	8.0	277	124	BB041356	BB041356 BB041356
12	c	19	8.0	289	127	BB157323	BB157323 BB157323
13		19	8.0	562	233	AQ763648	AQ763648 HS_2272_A
14		19	8.0	627	154	BG512632	BG512632 dad30f06.
15		19	8.0	735	106	AU003894	AU003894 AU003894
16		19	8.0	906	140	BE793639	BE793639 601588703
17	c	18	7.6	248	163	BE100728	BE100728 UI-R-BJ1-
18	c	18	7.6	273	129	AW799673	AW799673 PM2 CM005
19	c	18	7.6	336	13	AA882181	AA882181 vx38g12.r
20		18	7.6	360	157	D68826	D68826 CELK056H8F
21		18	7.6	374	235	AQ927830	AQ927830 RPCI-23-2
22		18	7.6	396	10	AA638305	AA638305 vl98a01.r
23		18	7.6	399	14	AA982673	AA982673 uh12a06.r
24		18	7.6	420	123	AW997626	AW997626 RC6 BN005
25	c	18	7.6	439	147	BF320551	BF320551 uz54d06.x
26		18	7.6	452	233	AQ769815	AQ769815 HS_3170_B
27		18	7.6	456	6	AA395958	AA395958 vb40e05.r
28		18	7.6	458	3	AA217593	AA217593 mu98g04.r
29	c	18	7.6	471	166	BE369495	BE369495 601220924
30		18	7.6	472	1	AA000313	AA000313 mg34e06.r
31		18	7.6	491	20	AI479037	AI479037 tm30e09.x
32		18	7.6	507	111	AW081540	AW081540 xc42e12.x
33	c	18	7.6	518	212	AZ351122	AZ351122 1M0089B01
34	c	18	7.6	551	20	AI464316	AI464316 mc65h11.x
35		18	7.6	554	244	AZ462968	AZ462968 1M0271I01
36		18	7.6	570	123	AW997624	AW997624 RC6 BN005
37	c	18	7.6	578	30	AV442805	AV442805 AV442805
38		18	7.6	586	12	AA795443	AA795443 vv20b12.r
39	c	18	7.6	618	223	AQ056672	AQ056672 CIT-HSP-2
40		18	7.6	642	12	AA791966	AA791966 vm79a01.r
41		18	7.6	696	168	BF677531	BF677531 602085796
42		18	7.6	726	169	BF780782	BF780782 602103059
43	c	18	7.6	792	10	AA697914	AA697914 HL03450.5
44		18	7.6	913	144	BF100686	BF100686 601753890
45		18	7.6	1330	192	AK012630	AK012630 Mus muscu
46		18	7.6	1621	151	BF667548	BF667548 602120714
47	c	18	7.6	1802	192	AK018490	AK018490 Mus muscu
48		18	7.6	1966	192	AK013258	AK013258 Mus muscu
49	c	18	7.6	2133	154	BG493715	BG493715 602542744
50		17	7.1	166	5	AA339955	AA339955 EST45123

ALIGNMENTS

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RESULT 1
BE410697
LOCUS       BE410697      646 bp    mRNA            EST       21-JUL-2000
DEFINITION  601300763F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:3635511 5',
            mRNA sequence.
ACCESSION   BE410697
VERSION     BE410697.1  GI:9347147
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 646)
  AUTHORS   NIH MGC http://[illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: Ling Hong/Rubin Laboratory
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: [illegible]
            Plate: LLCM:31  row: m  column: 16
            High quality sequence start: 27
            High quality sequence stop: 644.
FEATURES             Location/Qualifiers
     source          1..646
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "IMAGE:3635511"
                     /clone_lib "NIH_MGC_21"
                     /tissue_type "choriocarcinoma"
                     /lab_host "DH10B (phage resistant)"
                     /note "Organ: placenta; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Size-selected [illegible]
                     for average insert size 1.8kb. Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT       96 a    208 c    217 g    124 t      1 others
ORIGIN

  Query Match              80.7%;  Score 192;  DB 167;  Length 646;
  Best Local Similarity   100.0%;  Pred. No. 4.4e-93;
  Matches  192;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 [illegible] 60
Db        455 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGGCCGTG[illegible] 514

Qy         61 [illegible] 120
Db        515 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCC[illegible] 574

Qy        121 [illegible] 180
Db        575 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGGCTGA[illegible] 634

Qy        181 ggaggaggacgg 192
Db        635 GGAGGAGGACGG 646


RESULT 2
AA634317/c
LOCUS       AA634317      281 bp    mRNA            EST       [illegible]
DEFINITION  zu78c05.s1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE:744[illegible]
            3', mRNA sequence.
ACCESSION   AA634317
VERSION     AA634317.1  GI:2557531
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 281)
  AUTHORS   Hillier,L., Allen,M., Bowles,L., Dubuque,T., [illegible]
            Kriaman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
            ,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
            White,Y., Wylie,T., Waterston,R. and Wilson,R.
```

```
  TITLE     WashU-NCI human EST Project
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Wilson RK
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            This clone is available royalty free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 167.
FEATURES             Location/Qualifiers
     source          1..281
                     /organism="Homo sapiens"
                     /db_xref="GDB:5931598"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:744128"
                     /clone_lib="Soares_testis_NHT"
                     /sex="male"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA
                     was prepared from mRNA obtained from Clontech Laboratories
                     , Inc., and primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCCCAATTTTTTTTTTTTTTTTT 3'].
                     Double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. Library
                     went through one round of normalization to Cot5, and was
                     constructed by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       71 a     71 c     79 g     60 t
ORIGIN

  Query Match            71.4%;  Score 170;  DB 10;  Length 281;
  Best Local Similarity   99.5%;  Pred. No. 3.5e-81;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        247 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGCCT 188

Qy         61 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctccc 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||| |
Db        187 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 128

Qy        121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        127 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCGCT 68

Qy        181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
              |||||||||||||||||||||||||||||||||||||||||
Db         67 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 27


RESULT      3
AI218223/c
LOCUS       AI218223     359 bp    mRNA            EST       30-NOV-1998
DEFINITION  qh23a03.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone
            IMAGE:1845484 3' similar to TR:P78358 P78358 AUTOIMMUNOGENIC
            CANCER/TESTIS ANTIGEN NY-ESO-1. ;, mRNA sequence.
ACCESSION   AI218223
VERSION     AI218223.1  GI:3798038
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 359)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            Insert Length: 793   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 270.
FEATURES             Location/Qualifiers
     source          1..359
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1845484"
                     /clone_lib="Soares_NFL_T_GBC_S1"
                     /lab_host="DH10B"
                     /note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI.
                     Equal amounts of plasmid DNA from three normalized
                     libraries (fetal lung NbHL19W, testis NHT, and B-cell
                     NCI_CGAP_GCB1) were mixed, and ss circles were made in
                     vitro. Following HAP purification, this DNA was used as
                     tracer in a subtractive hybridization reaction. The driver
                     was PCR amplified cDNAs from pools of 5,000 clones made
                     from the same 3 libraries. The pools consisted of
                     I.M.A.G.E. clones 297480-302087, 682632-687239,
                     726408-728711, and 729096-731399. Subtraction by Bento
                     Soares and M. Fatima Bonaldo. "
BASE COUNT       90 a     94 c    109 g     66 t
ORIGIN

  Query Match            71.4%;  Score 170;  DB 17;  Length 359;
  Best Local Similarity   99.5%;  Pred. No. 3.5e-81;
  Matches  220;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtgtttttggctcaggct 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||| ||
Db        236 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTTGGCTCAGCCT 177

Qy         61 ccctcagggcagaggcgctaagcccagcctggcgccccttcctaggtcatgcctcctccc 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        176 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCCTTCCTAGGTCATGCCTCCTCCC 117

Qy        121 ctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcgct 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        116 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCGCT 57

Qy        181 ggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
              |||||||||||||||||||||||||||||||||||||||||
Db         56 GGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 16


RESULT      4
AL553954
LOCUS       AL553954     700 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL553954 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI025YI02 5
            prime, mRNA sequence.
ACCESSION   AL553954
VERSION     AL553954.1  GI:12894271
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 700)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
FEATURES             Location/Qualifiers
```

```
     source          1..700
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "CS0DI079YI02"
                     /clone_lib "LTI_NFL006_PL2"
                     /tissue_type "placenta"
                     /note "Vector: pCMVSPORT 6; Site 1: NotI, 1st strand cDNA
                     was primed with a NotI oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      114 a    213 c    239 g    132 t      2 others
ORIGIN

  Query Match             68.5%;  Score 163;  DB 106;  Length 700;
  Best Local Similarity   100.0%;  Pred. No. 2.2e-77;
  Matches  163;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         59 ctccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatgcctcctc 118
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        526 CTCCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCTTCCTAGGTCATGCCTCCTC 585

Qy        119 ccctagggaatggtcccagcacgagtggccagttcattgtggggcctgattgtttgtcg 178
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        586 CCCTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGGGCCTGATTGTTTGTCG 645

Qy        179 ctggaggaggacggcttacatgtttgtttctgtagaaaataaa 221
              |||||||||||||||||||||||||||||||||||||||||||
Db        646 CTGGAGGAGGACGGCTTACATGTTTGTTTCTGTAGAAAATAAA 688


RESULT    5
AL553953/c
LOCUS       AL553953        629 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL553953 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI079YI02 5
            prime, mRNA sequence.
ACCESSION   AL553953
VERSION     AL553953.1  GI:12894269
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 629)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
FEATURES             Location/Qualifiers
     source          1..629
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "CS0DI079YI02"
                     /clone_lib "LTI_NFL006_PL2"
                     /tissue_type "placenta"
                     /note "Vector: pCMVSPORT 6; Site 1: NotI, 1st strand cDNA
                     was primed with a NotI oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      108 a    220 c    202 g     98 t      1 others
ORIGIN

  Query Match             46.2%;  Score 110;  DB 106;  Length [illegible];
  Best Local Similarity   99.4%;  Pred. No. 1.1e-48;
  Matches  160;  Conservative    0;  Mismatches    1;  Indels    [illegible];  Gaps    [illegible];

Qy          1 cagctttccctgttgatgtggatcacgcagtgctttctgcccgtatttt[illegible]
              |||||||||||||||||||||||||||||||||||||||||||||||||[illegible]
Db        162 CAGCTTTCCCTGTTGATGTGGATCACGCAGTGCTTTCTGCCCG[illegible]

Qy         61 ccctcagggcagaggcgctaagcccagcctggcgcccttcctaggtcatgcc[illegible]
              ||||||||||||||||||||||||||||||||||||||||||||||||||||[illegible]
Db        102 CCCTCAGGGCAGAGGCGCTAAGCCCAGCCTGGCGCCCTTCCTAG[illegible]

Qy        121 ctagggaatggtcccagcacgagtggccagttcattgtggg 161
              |||||||||||||||||||||||||||||||||||||||||
Db         42 CTAGGGAATGGTCCCAGCACGAGTGGCCAGTTCATTGTGGG 2


RESULT    6
BE385880/c
LOCUS       BE385880        852 bp    mRNA            EST       [illegible]
DEFINITION  601275548F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:[illegible]
            mRNA sequence.
ACCESSION   BE385880
VERSION     BE385880.1  GI:9331245
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 852)
  AUTHORS   NIH MGC http://[illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs@mail.nih.gov
            Tissue Procurement: ATCC/[illegible]/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM283  row: o  column: 12
            High quality sequence start: 14
            High quality sequence stop: 520.
FEATURES             Location/Qualifiers
     source          1..852
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "IMAGE:[illegible]"
                     /clone_lib "NIH_MGC_20"
                     /tissue_type "melanotic melanoma"
                     /lab_host "DH10B (phage resistant)"
                     /note "Organ: skin; Vector: pCMV-SPORT6; Site 1: [illegible]
                     EcoRI; cDNA made by oligo-dT priming. Directionally
                     cloned into EcoRI/XhoI sites using [illegible]
                     adaptor: GGCACGAG(G). Size-selected [illegible]
                     insert size 1.8kb. Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using ZAP cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      196 a    250 c    257 g    149 t
ORIGIN

  Query Match             27.7%;  Score 66;  DB 167;  Length [illegible];
  Best Local Similarity   100.0%;  Pred. No. 7.2e-25;
  Matches   66;  Conservative    0;  Mismatches    0;  Indels    [illegible];  Gaps    [illegible];
```

```
Qy       16 atgtggatcacgcagtgctttctgcccgtgttttggctcaggctccctcagggcagagg 75
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      217 ATGTGGATCACGCAGTGCTTTCTGCCCGTGTTTTGGCTCAGGCTCCCTCAGGGCAGAGG 158

Qy       76 cgctaa 81
            ||||||
Db      157 CGCTAA 152


RESULT   7
BG575764
LOCUS       BG575764       770 bp    mRNA             EST       10-APR-2001
DEFINITION  602597257F1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:4705839 5',
            mRNA sequence.
ACCESSION   BG575764
VERSION     BG575764.1  GI:13583417
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 770)
  AUTHORS   NIH-MGC http://[illegible]
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10573  row: b  column: 16
            High quality sequence stop: 713.
FEATURES             Location/Qualifiers
     source          1..770
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4705839"
                     /clone_lib="NIH_MGC_87"
                     /tissue_type="mammary adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: breast. Vector: pCMV-SPORT6. Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.383 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      135 a    231 c    270 g    134 t
ORIGIN


  Query Match             10.5%;  Score 25;  DB 155;  Length 770;
  Best Local Similarity   100.0%;  Pred. No. 0.011;
  Matches   25;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy       15 gatgtggatcacgcagtgctttctg 39
            |||||||||||||||||||||||||
Db      719 GATGTGGATCACGCAGTGCTTTCTG 743


RESULT   8
AA866133/c
LOCUS       AA866133       148 bp    mRNA             EST       13-MAY-1998
DEFINITION  oh53d09.s1 NCI_CGAP_GC4 Homo sapiens cDNA clone IMAGE:1470353 3'
            similar to TR:[illegible] ANTIGEN
            NY-ESO-1. ;, mRNA sequence.
ACCESSION   AA866133
VERSION     AA866133.1  GI:2958409
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 148)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html

            Trace considered overall poor quality
            Insert Length: 410   Std Error: 0.00
            Seq primer: -40m13 fwd. ET from Amersham
            High quality sequence stop: 1.
FEATURES             Location/Qualifiers
     source          1..148
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:1470353"
                     /clone_lib="NCI_CGAP_GC4"
                     /tissue_type="pooled germ cell tumors"
                     /lab_host="DH10B"
                     /note="Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; 1st strand cDNA was prepared from 3 pooled
                     germ cell tumors, and was then primed with a Not I -
                     oligo(dT) primer. Double stranded cDNA was ligated to Eco
                     RI adaptors (Pharmacia), digested with Not I and cloned
                     into the Not I and Eco RI sites of the modified pT7T3
                     vector. Library is normalized. Library was constructed by
                     Bento Soares and M. Fatima Bonaldo. "
BASE COUNT       17 a     30 c     48 g     25 t
ORIGIN


  Query Match             9.7%;  Score 23;  DB 11;  Length 148;
  Best Local Similarity   100.0%;  Pred. No. 0.13;
  Matches   23;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        2 [illegible] 24
            |||||||||||||||||||||||
Db       69 AGCTTTCCCTGTTGATGTGGATC 47


RESULT   9
AZ312149
LOCUS       AZ312149       603 bp    DNA              GSS       [illegible]
DEFINITION  1M0027A23R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
            clone UUGC1M0027A23 R, DNA sequence.
ACCESSION   AZ312149
VERSION     AZ312149.1  GI:10355811
KEYWORDS    GSS.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 603)
  AUTHORS   Dunn,D., Aoyagi,A., Barber,M., Beacorn,L., [illegible]
            Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,L., Reilly,
            [illegible]
            and Wright,D.,Weiss,R.
  TITLE     Mouse whole genome scaffolding with paired end reads from 10kb
            plasmid inserts
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Robert B. Weiss
            University of Utah Genome Center
```

```
            University of Utah
            Rm. 408, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
            84112, USA
            Tel: 801 585 5606
            Fax: 801 585 7177
            Email: ddunn@genetics.utah.edu
            Insert Length: 10000   Std Error: 0.00
            Plate: 0027  row: A  column: 23
            Seq primer: CACACAGGAAACAGCTATGACC
            Class: plasmid ends
            High quality sequence stop: 603.
FEATURES             Location/Qualifiers
     source          1..603
                     /organism "Mus musculus"
                     /strain "C57BL/6J"
                     /db_xref "taxon:10090"
                     /clone "[illegible]"
                     /clone_lib "Mouse 10kb plasmid [illegible] library"
                     /sex "Male"
                     /lab_host "E. Coli strain XL10 Gold, Tl-resistant, F-"
                     /note "Vector: pWD42e7; Purified genomic DNA from M.
                     musculus C57BL/6J (male) was obtained from the Jackson
                     Laboratory Mouse DNA Resource
                     (http://www.[illegible]) DNA
                     was hydrodynamically sheared by repeated passage through a
                     0.005 inch orifice at constant velocity. The sheared DNA
                     was blunt end repaired with T4 DNA polymerase and T4
                     polynucleotide kinase. Adaptor oligonucleotides were
                     ligated to the blunt ends in high molar excess. The
                     adaptored DNA was purified and size-selected for a 9.5 to
                     10.5 kb range using preparative agarose gel
                     electrophoresis. Vector DNA was prepared from a derivative
                     of pWD42 (gi|4732114|gb|AF129072.1), a copy-number
                     inducible derivative of plasmid R1. The vector was ligated
                     with adaptors complementary to the insert adaptors and
                     purified. The sheared, adaptored mouse DNA was annealed to
                     adaptored vector DNA, and transformed into
                     chemically-competent E. coli XL10 Gold (Stratagene) cells
                     and selected for ampicillin resistance."
BASE COUNT      216 a    117 c    113 g    157 t
ORIGIN

  Query Match              8.4%;  Score 20;  DB 241;  Length 603;
  Best Local Similarity   100.0%;  Pred. No. 5.7;
  Matches   20;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        211 tagaaataaagctgagcta 230
              ||||||||||||||||||||
Db        247 TAGAAAATAAAGCTGAGCTA 266

RESULT 10
BB056458/c
LOCUS       BB056458        261 bp    mRNA            EST       25-JUN-2000
DEFINITION  BB056458 RIKEN full-length enriched, 12 days embryo male wolffian
            duct Mus musculus cDNA clone 6720490N13 3' similar to M80956 Mus
            musculus calcium binding protein (pp52) mRNA, mRNA sequence.
ACCESSION   BB056458
VERSION     BB056458.1  GI:8463506
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 261)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Nakakube,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,[illegible]
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,[illegible]
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,[illegible]
            , Yano,F., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., [illegible]
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN) Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81 298 36 9013
            Fax: +81 298 36 9098
            Email: genome-res@rtc.riken.go.jp
            URL:[illegible]
            Carninci,P., Nishiyama,Y., Westover,A., [illegible]
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), [illegible] (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., [illegible]
            [illegible]
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.[illegible]) for
            further details.
FEATURES             Location/Qualifiers
     source          1..261
                     /organism "Mus musculus"
                     /strain "C57BL/6J"
                     /db_xref "taxon:10090"
                     /clone "6720490N13"
                     /clone_lib "RIKEN full-length enriched, 12 days embryo
                     male wolffian duct"
                     /sex "male"
                     /tissue_type "wolffian duct includes [illegible]"
                     /dev_stage "12 days embryo"
                     /lab_host "DH10B"
                     /note "Site 1: SalI; Site 2: BamHI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTTVN 3'] cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap trapper. Second strand cDNA was prepared with the
                     primer adapter of sequence [5'
                     GAGAGAGAGATCTCGAGTAATAAATTAATC[illegible] 3'] cDNA
                     was cloned into the XhoI and BamHI sites. Vector is a
                     modified pBluescript KS(+) after bulk excision from lambda
                     FLC 1. Cloning sites, 5' end: SalI; 3' end: BamHI"
BASE COUNT       64 a     84 c     47 g     66 t
ORIGIN

  Query Match              8.0%;  Score 19;  DB 124;  Length 261;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        117 tccctagggaatggtccc 135
              |||||||||||||||||||
Db        106 [illegible]TAGGGAATG[illegible] 88
```

```
RESULT 11
BB041356/c
LOCUS       BB041356      277 bp    mRNA            EST       23-JUN-2000
DEFINITION  BB041356 RIKEN full-length enriched, 13 days embryo male testis Mus
            musculus cDNA clone 6030455E12 3' similar to M89956 Mus musculus
            calcium binding protein (pp52) mRNA, mRNA sequence.
ACCESSION   BB041356
VERSION     BB041356.1  GI:8447742
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 277)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kajiwa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Fujimo,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,K., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome_res@rtc.riken.go.jp
            URL:http://genome.rtc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
             Please visit our web site (http://genome.rtc.riken.go.jp/) for
            further details.
FEATURES             Location/Qualifiers
     source          1..277
                     /organism="Mus musculus"
                     /strain="C57BL/6J"
                     /db_xref="taxon:10090"
                     /clone="6030455E12"
                     /clone_lib="RIKEN full-length enriched, 13 days embryo
                     male testis"
                     /sex="male"
                     /tissue_type="testis"
                     /dev_stage="13 days embryo"
                     /lab_host="DH10B"
                     /note="Site_1: SalI, Site_2: BamHI. cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN. Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full-length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot = 5.0 and subtraction to Rot = 100.0. Second strand
                     cDNA was prepared with the primer adapter of sequence [5'
                     GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCC 3'], cDNA
                     was cloned into the XhoI and BamHI sites. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC 1. Cloning sites, 5' end: SalI; 3' end: BamHI."
BASE COUNT       62 a     80 c     58 g     77 t
ORIGIN

  Query Match              8.0%;  Score 19;  DB 124;  Length 277;
  Best Local Similarity  100.0%;  Pred. No. 19;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy        117 cccttaataattatcc 135
              |||||||||||||||||||
Db        115 CCCCTTAATTAATTTAATGGTCCC 97


RESULT 12
BB157323/c
LOCUS       BB157323      289 bp    mRNA            EST       27-JUN-2000
DEFINITION  BB157323 RIKEN full-length enriched, 16 days neonate thymus Mus
            musculus cDNA clone A130035M02 3' similar to M89956 Mus musculus
            calcium binding protein (pp52) mRNA, mRNA sequence.
ACCESSION   BB157323
VERSION     BB157323.1  GI:8813253
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 289)
  AUTHORS   Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
            ,P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N.,
            Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
            Izawa,M., Kadota,K., Kajiwa,I., Kai,C., Kawai,J., Kikuchi,N.,
            Kiyosawa,H., Fujimo,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M.
            , Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.
            , Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
            ,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y.
            , Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toya
            ,T., Tsunoda,Y., Watahiki,A., Watanabe,S., Yamamura,T., Yamanaka,I.
            , Yano,K., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino
            ,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     RIKEN Mouse ESTs (Konno,H., et al.)
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Yoshihide Hayashizaki
            Genome Exploration Research Group, Life Science Tsukuba Center,
            Genome Science Laboratory
            The Institute of Physical and Chemical Research (RIKEN), Genomic
            Sciences Center
            3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
            Tel: +81-298-36-9013
            Fax: +81-298-36-9098
            Email: genome_res@rtc.riken.go.jp
            URL:http://genome.rtc.riken.go.jp/
            Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasaki
            ,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
            Thermostabilization and thermoactivation of thermolabile enzymes by
            trehalose and its application for the synthesis of full length
            cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
             Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J.,
            Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki
            ,Y. and Hayashizaki,Y.
             Automated filtration-based high-throughput plasmid preparation
            system. Genome Res. 9 (5), 463-470 (1999)
             Carninci,P. and Hayashizaki,Y.
             High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
            19-44 (1999)
```

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            Please visit our web site (http://www.xx.xx.xx/) for
            further details.
FEATURES             Location/Qualifiers
     source          1. .289
                     /organism "Mus musculus"
                     /db_xref "taxon:10090"
                     /clone "A1000405M02"
                     /clone_lib "RIKEN full length enriched, 16 days neonate
                     thymus"
                     /tissue_type "thymus"
                     /dev_stage "16 days neonate"
                     /lab_host "DH10B"
                     /note "Site_1: SalI; Site_2: PmeI; cDNA library was
                     prepared and sequenced in Mouse Genome Encyclopedia
                     Project of Genome Exploration Research Group in Riken
                     Genomic Sciences Center and Genome Science Laboratory in
                     RIKEN, Division of Experimental Animal Research in Riken
                     contributed to prepare mouse tissues. 1st strand cDNA was
                     primed with a primer [5'
                     GAGAGAGAGAAGGAICCAAGAGCICTTTTTTTTTTTTTTTTVN 3'], cDNA was
                     prepared by using trehalose thermo-activated reverse
                     transcriptase and subsequently enriched for full length by
                     cap-trapper. cDNA went through one round of normalization
                     to Rot  10.0 and subtraction to Rot  185.). Second
                     strand cDNA was prepared with the primer adapter of
                     sequence [5' GAGAGAGAGATTCTGAITAATTAAATTAATGCGCCCCCCCCCC
                     3']. cDNA was cleaved with XhoI and BamHI. Vector: a
                     modified pBluescript KS(+) after bulk excision from Lambda
                     FLC 1."
BASE COUNT        69 a      99 c      48 g      73 t
ORIGIN


  Query Match              8.0%;  Score 19;  DB 127;  Length 289;
  Best Local Similarity   100.0%;  Pred. No. 19;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     117 tcccctaqqqaatqqtccc 135
           |||||||||||||||||||
Db     134 TCCCCTAGGGAATGGTCCC 116


RESULT  14
AQ763648
LOCUS       AQ763648       562 bp    DNA             GSS       28-JUL-1999
DEFINITION  BS_3232_A1_C05_1?? CIT Approved Human Genomic Sperm Library D Homo
            sapiens genomic clone Plate=3232 Col 9 Row=M, DNA sequence.
ACCESSION   AQ763648
VERSION     AQ763648.1  GI:5641764
KEYWORDS    GSS.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 562)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones may be purchased from Research Genetics (info@resgen.com).
            BAC end Web Server:  http://www.tigr.org/bac
            Plate: 3232  row: M  column: 9
            Seq primer: 17
            Class: BAC ends
            High quality sequence stop: 562
FEATURES             Location/Qualifiers
     source          1. .562
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone "Plate 3232 Col 9 Row M"
                     /clone_lib "CIT Approved Human Genomic Sperm Library D"
                     /sex "male"
                     /note "organ: sperm; Vector: pBeloBAC11; BAC Cloning 2.
                     E Coli DH10B"
BASE COUNT       130 a     125 c     105 g     184 t      DB: Others
ORIGIN


  Query Match              8.0%;  Score 19;  DB 233;  Length 562;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     165 ctqattqttttqtcqctqqa 184
           |||||||||||||||||||
Db      74 CTGATTGTTTGTCGCTGGA 92


RESULT  14
BG512642
LOCUS       BG512642       627 bp    mRNA            EST       28-MAR-...
DEFINITION  da43ut06.x1 Wellcome CRC pCS107 tropicalis stg ... Silurana
            tropicalis cDNA clone IMAGE:4441114 3', mRNA sequence.
ACCESSION   BG512642
VERSION     BG512642.1  GI:13483289
KEYWORDS    EST.
SOURCE      western clawed frog.
  ORGANISM  Silurana tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Silurana.
REFERENCE   1  (bases 1 to 627)
  AUTHORS   Clifton,S., Johnson,S.L., Blumberg,B., Sater,A
            , Martin,J., Wylie,C., Underwood,K., Theisen,M., Bowers,Y., Pete
            ,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,J., McCann,K.,
            Waterston,R. and Wilson,R.
  TITLE     WashU Xenopus EST project, 1999
  JOURNAL   Unpublished (1999)
COMMENT     Other_ESTs: da43ut06.y1
            Contact: Sandy Clifton, Ph.D.
            WashU Xenopus EST project, 1999
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library constructed by A. Zorn and J. Mason (Wellcome/CRC Institute
            ). DNA Sequencing by: Washington University Genome Sequencing
            Center
            Clone distribution: Xenopus clones from this library are available
            through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 499.
FEATURES             Location/Qualifiers
     source          1. .627
                     /organism "Silurana tropicalis"
                     /db_xref "taxon:8364"
                     /clone "IMAGE:4441114"
                     /clone_lib "Wellcome CRC pCS107 tropicalis stg ... cDNA 1."
                     /tissue_type "whole embryo, stages ... "
                     /lab_host "DH10B (phage resistant)"
                     /note "Vector: pCS107; Site_1: Not I; Site_2: Sal I; cDNAs
                     were oligo-dT primed and directionally cloned. Average
                     insert size 1.5 kb, range 0.5-4 kb. Library constructed by
                     A. Zorn and J. Mason (Wellcome/CRC Institute). "
BASE COUNT       160 a     144 c     126 g     197 t
ORIGIN
```

```
  Query Match              8.0%;  Score 19;  DB 154;  Length 627;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     201 tttqtttctgtagaaaata 219
           |||||||||||||||||||
Db     116 TTTGTTTCTGTAGAAAATA 134


RESULT  15
AU003894
LOCUS       AU003894      735 bp    mRNA            EST       19 JAN 1999
DEFINITION  AU003894 Bombyx mori p50(Daizo) Bombyx mori cDNA clone ws00713,
            mRNA sequence.
ACCESSION   AU003894
VERSION     AU003894.1  GI:4161265
KEYWORDS    EST.
SOURCE      domestic silkworm.
  ORGANISM  Bombyx mori
            Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
            Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia
            ; Bombycoidea; Bombycidae; Bombyx.
REFERENCE   1  (bases 1 to 735)
  AUTHORS   Mita,K., Morin,S.M., Shimada,T., Banno,Y. and Maeda,S.
  TITLE     Establishment of cDNA database of Bombyx mori
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Mita K
            Genome Research Group
            National Institute of Radiological Sciences
            Anagawa 4-9-1, Inage, Chiba 263-8555, Japan
            Email: kmita@nirs.go.jp
            PROJECT = 'CREST project by JST'.
FEATURES             Location/Qualifiers
     source          1..735
                     /organism="Bombyx mori"
                     /strain "p50(Daizo)"
                     /db_xref="taxon:7091"
                     /clone="ws00713"
                     /clone_lib="Bombyx mori p50(Daizo)"
BASE COUNT      240 a    102 c    119 g    272 t
ORIGIN

  Query Match              8.0%;  Score 19;  DB 106;  Length 735;
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     202 ttqtttctgtagaaaataa 220
           |||||||||||||||||||
Db     153 TTGTTTCTGTAGAAAATAA 171


RESULT  16
BE793639
LOCUS       BE793639      906 bp    mRNA            EST       20-SEP-2000
DEFINITION  601588703F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3942889 5',
            mRNA sequence.
ACCESSION   BE793639
VERSION     BE793639.1  GI:10214746
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 906)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/
  TITLE     National Institutes of Health Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: DCTD/DTP
            cDNA Library Preparation: Lind Bond/Rubin Laboratory
            cDNA Library Arrayed by: the I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Plate: LLCM797  row: e  column: 02
            High quality sequence stop: 765.
FEATURES             Location/Qualifiers
     source          1..906
                     /organism "Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone "IMAGE:3942889"
                     /clone_lib "NIH_MGC_7"
                     /tissue_type "small cell carcinoma"
                     /cell line "M603"
                     /lab_host "DH10B (phage-resistant)"
                     /note "Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
                     EcoRI; cDNA made by oligo dT priming. Size-selected cDNA
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G). Size-selected cDNA; 1.8 kb mean
                     insert size 1.8kb. Library constructed by Lind Bond in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using SAP cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
BASE COUNT      158 a    294 c    278 g    216 t
ORIGIN

  Query Match              8.0%;  Score 19;  DB 140;  Length [illegible];
  Best Local Similarity   100.0%;  Pred. No. 20;
  Matches   19;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      49 ttqqctcaqactcccctcaq 67
           |||||||||||||||||||
Db     677 TTGGCTCAGGCTCCCTCAG 695


RESULT  17
BE100728/c
LOCUS       BE100728      248 bp    mRNA            EST       15-JAN-2000
DEFINITION  UI-R-BJ1-ata-c-09-0-UI.s1 UI-R-BJ1 Rattus norvegicus cDNA clone
            UI-R-BJ1-ata-c-09-0-UI 3', mRNA sequence.
ACCESSION   BE100728
VERSION     BE100728.1  GI:8492591
KEYWORDS    EST.
SOURCE      Norway rat.
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 248)
  AUTHORS   Bonaldo,M.F., Lennon,G. and Soares,M.B.
  TITLE     Normalization and subtraction: two approaches to facilitate gene
            discovery
  JOURNAL   Genome Res. 6 (9), 791-806 (1996)
  MEDLINE   97044477
COMMENT     Contact: Soares, MB
            Program for Rat Gene Discovery and Mapping
            University of Iowa
            451 Eckstein Medical Research Building Iowa City, IA 52242 USA
            Tel: 319 335 8250
            Fax: 319 335 9565
            Email: msoares@blue.weeg.uiowa.edu
            The sequence contained an oligo-dT track that was present in the
            oligonucleotide that was used to prime the synthesis of first
            strand cDNA and therefore this may represent a genuine poly A
            tail. The sequence tag present in the cDNA between the NotI site
            and the oligo dT track served to identify it as a clone [illegible]
            normalized AV canal at 16.5 dpe library cDNA Library Preparation:
            M.B. Soares Lab Clone distribution: clones will be available
            through Research Genetics (www.resgen.com)
            Seq primer: M13 Forward
            POLYA Yes.
```

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FEATURES             Location/Qualifiers
     source          1..248
                     /organism "[illegible]"
                     /strain "Sprague-Dawley"
                     /db_xref "taxon:10116"
                     /clone "UI-R-BJ1-atu-c-09-0-UI"
                     /clone_lib "UI-R-BJ1"
                     /lab_host "DH10B (Life Technologies)"
                     /note "Vector: pT7T3D-Pac (Pharmacia) with a modified
                     polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-BJ1
                     library is a subtracted library derived from the following
                     tissues: atrium at 16.5 dpc, ventricle at 16.5 dpc, AV
                     canal at 16.5 dpc, atrium at 15 dpc, ventricle at 15 dpc,
                     AV canal at 15 dpc, ventricle at 13 dpc, and adult heart.
                     For a detailed description of the library from which this
                     clone was derived, please visit our web site at
                     ratest.cnqr.uiowa.edu. The subtraction has been previously
                     described in (Bonaldo, Lennon and Soares, Genome Research
                     6:791-806, 1996)
                     IAG_LIB:UI-R-BJ1
                     IAG_TISSUE:AV canal at 16.5 dpc
                     IAG_SEQ:GAACC"
BASE COUNT        91 a      44 c      80 g      84 t
ORIGIN

  Query Match           7.6%;  Score 18;  DB 164;  Length 248;
  Best Local Similarity   100.0%;  Pred. No. 67;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     195 tacatgtttgtttctata 212
           ||||||||||||||||||
Db     189 TACATGTTTGTTTCTGTA 172


RESULT 18
AW799673/c
LOCUS       AW799673      273 bp    mRNA            EST       16-MAY-2000
DEFINITION  PM2-UM0053-240500-005-f02 UM0053 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW799673
VERSION     AW799673.1  GI:7851543
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 273)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Tozzo,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brumstein,A., de Oliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55 11 2704922
            Fax: +55 11 2707951
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAIRE/CAGE Human Cancer Genome
            Project. This entry can be seen in the following URL
            [illegible]
            400-005-f02&33 2000-03-24&14 1)
            Seq primer: puc 18 forward
            High quality sequence start: 20
            High quality sequence stop: 273.
FEATURES             Location/Qualifiers
     source          1..273
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
                     /clone_lib "UM0053"
                     /dev_stage "Adult"
                     /note "Organ: uterus; Vector: pcDNA I/Amp; Site_1: Not I;
                     Sma1; A mini-library was made by cleaned products derived
                     from  ORESTES PCR (U.S. Letters Patent application No. [illegible]
                     ,716    Ludwig Institute for Cancer Research) profiles
                     into  the pDC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under l o
                     stringency conditions."
BASE COUNT       103 a      81 c      62 g      27 t
ORIGIN

  Query Match           7.6%;  Score 18;  DB 120;  Length 273;
  Best Local Similarity   100.0%;  Pred. No. 68;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     193 ttacatgtttgtttctgt 210
           ||||||||||||||||||
Db     141 CTTACATGTTTGTTTCTG 124


RESULT 19
AA882181/c
LOCUS       AA882181      336 bp    mRNA            EST       [illegible] MAY-1996
DEFINITION  vs48d12.r1 Stratagene mouse lung 937302 Mus musculus cDNA cl to
            IMAGE:1277542 5', mRNA sequence.
ACCESSION   AA882181
VERSION     AA882181.1  GI:2991292
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
REFERENCE   1  (bases 1 to 336)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Labuspes[illegible]
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin, [illegible] Morris M.,
            Schellenberg,K., Stoptoe,M., Tan F., Underwood,K., Moore,R.,
            Theisiat,R., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
  TITLE     The WashU-HHMI Mouse EST Project
  JOURNAL   Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU HHMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, P x 8501, St. Louis, MO [illegible]
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through [illegible] to
            IMAGE Consortium (info@image.llnl.gov) for [illegible] use.
            MCI:669442
            Putative full length read
            Vector to vector length is 750
            Seq primer:  28mlk rsvl RI from Amersham
            High quality sequence stop: 324.
FEATURES             Location/Qualifiers
     source          1..336
                     /organism "Mus musculus"
                     /strain "C57Bl/6 x CBA"
                     /db_xref "taxon:10090"
                     /clone "IMAGE:1277542"
                     /clone_lib "Stratagene mouse lung [illegible]"
                     /sex "female"
                     /tissue_type "lung"
                     /dev_stage "6-8 month old"
                     /lab_host "SOLR (kanamycin resistant)"
                     /note "Organ: lung; Vector: pBluescript SK-; Site 1: [illegible]
                     ; Site 2: XhoI; Cloned unidirectionally; [illegible] primer; [illegible]
                     dl, 6-8 month old female lung and [illegible] were [illegible]
```

were source of mRNA. Average insert size: 1.5 kb; Mul-ZAP
XR Vector: 5' adaptor sequence: 5' GAATTCGGCACGAG 3' 3'
adaptor sequence: 5' CTCGACTTTTTTTTTTTTTTTT 3'"
BASE COUNT 79 a 93 c 99 g 66 t
ORIGIN

Query Match 7.6%; Score 18; DB 13; Length 336;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 50 tgactcaggctcctcaag 67
||||||||||||||||||
Db 223 TGGCTCAGGCTCCCTCAG 206

RESULT 20
D68826
LOCUS D68826 360 bp mRNA EST 07-DEC-1995
DEFINITION CEK056B8F Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk56h8 5', mRNA sequence.
ACCESSION D68826
VERSION D68826.1 GI:1104533
KEYWORDS EST.
SOURCE Caenorhabditis elegans.
ORGANISM Caenorhabditis elegans
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 360)
AUTHORS Kohara,Y., Mitsuki,H., Nishigaki,A., Mori Ishi,T., Kojima,A. and Tabata,M.
TITLE Toward an expression map of the C.elegans genome
JOURNAL Unpublished (1994)
COMMENT Contact: Yuji Kohara
Gene Library Lab
National Institute of Genetics
Yata 1111, Mishima, Shizuoka 411, Japan
Tel: 81-559-81-6854
Fax: 81-559-81-6855
Email: ykohara@lab.nig.ac.jp.
FEATURES Location/Qualifiers
source 1..360
/organism="Caenorhabditis elegans"
/strain="CB1489 him-8(e1489)"
/db_xref="taxon:6239"
/clone="yk56h8"
/clone_lib "Yuji Kohara unpublished cDNA"
/sex="hermaphrodite male"
/tissue_type="whole animal"
/dev_stage="varied"
BASE COUNT 101 a 112 c 87 g 56 t 4 others
ORIGIN

Query Match 7.6%; Score 18; DB 157; Length 360;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 175 gtcgctgcaggacgaccg 192
||||||||||||||||||
Db 278 GTCGCTGCAGGACGACCG 295

RESULT 21
AQ927830
LOCUS AQ927830 374 bp DNA GSS 21-DEC-1999
DEFINITION RPCI-23 262A18.TJ RPCI-23 Mus musculus genomic clone RPCI-23-262A18, DNA sequence.
ACCESSION AQ927830
VERSION AQ927830.1 GI:6616823
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 374)
AUTHORS Zhao,S., Nierman,W., Feldblyum,T., Malek,J., Shatsman,S., Akiyama,B., Levins,M., Mcgann,S., Tsegaye,G., Geer,K., Khouri,H., de Vanzo,N. and Fraser,C.M.
TITLE Mouse BAC End Sequences from Library RPCI-23
JOURNAL Unpublished (1999)
COMMENT Other_GSSs: RPCI-23-262A18.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/orderinginfo.htm) or from Research Genetics (info@resgen.com). BAC end pairs: http://www.tigr.org/tdb/mdb/BAC_ends/bac_end_intro.html
Plate: 262 row: A column: 18
Seq primer: T7
Class: BAC ends.
FEATURES Location/Qualifiers
source 1..374
/organism "Mus musculus"
/strain "C57BL/6J"
/db_xref "taxon:10090"
/clone "RPCI-23-262A18"
/clone_lib="RPCI-23"
/sex "Female"
/lab_host="DH10B"
/note "Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI; Female C57BL/6J mouse kidney and brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBACe3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 119 a 65 c 57 g 133 t
ORIGIN

Query Match 7.6%; Score 18; DB 235; Length 374;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 209 tgtgtaaaataaagctga 226
||||||||||||||||||
Db 206 TGTAGAAAATAAAGCTGA 223

RESULT 22
AA638305
LOCUS AA638305 296 bp mRNA EST 22-OCT-1997
DEFINITION vl98a01.r1 Knowles Solter mouse blastocyst B1 Mus musculus cDNA clone IMAGE:988680 5' similar to gb:D10727 Mouse mRNA for NFE-1 protein, complete cds (MOUSE);, mRNA sequence.
ACCESSION AA638305
VERSION AA638305.1 GI:2561893
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciuromorpha; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 296)
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Bonfiglio,N., Dietrich,S., Kucaba,T., Lacy,M., Le,M., Matthes,L., Morris,M., Schellenberg,K., Stoptoe,M., Tan,F., Underwood,K., Moore,B., Theisiau,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.

```
TITLE       The WashU-HHMI Mouse EST Project
 JOURNAL    Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:560960.
FEATURES             Location/Qualifiers
     source          1..396
                     /organism "Mus musculus"
                     /strain "B6C3 F1/J"
                     /db_xref "taxon:10090"
                     /clone "IMAGE:988680"
                     /clone_lib "Knowles Solter mouse blastocyst B1"
                     /tissue_type "blastocyst"
                     /dev_stage "embryo (pre-implantation)"
                     /lab_host "DH10B"
                     /note "Organ: embryo; Vector: pSPORT; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally from mRNA prepared
                     from 860 blastocysts.   Primer: SalI(dT):
                     5' CGGTCGACCGTCGACCGTTTTTTTTTTTTTTT-3'.  cDNAs were
                     cloned into the NotI/SalI sites of a pSPORT vector (Life
                     Technologies).  Two different size selections: B1 (larger
                     inserts) and B3."
BASE COUNT      103 a     70 c     92 g    131 t
ORIGIN

  Query Match              7.6%;  Score 18;  DB 10;  Length 396;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    199 tgtttgtttctgtagaaa 216
          ||||||||||||||||||
Db     84 TGTTTGTTTCTGTAGAAA 101


RESULT 23
AA982673
LOCUS       AA982673     399 bp    mRNA            EST       27-MAY-1998
DEFINITION  uh12a06.r1 Soares mouse hypothalamus NbHy Mus musculus cDNA clone
            IMAGE:1617682 5', mRNA sequence.
ACCESSION   AA982673
VERSION     AA982673.1  GI:3161332
KEYWORDS    EST.
SOURCE      house mouse.
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 399)
  AUTHORS   Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
            Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
            Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
            Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
            Waterston,R.
TITLE       The WashU-HHMI Mouse EST Project
 JOURNAL    Unpublished (1996)
COMMENT     Contact: Marra M/Mouse EST Project
            WashU-HHMI Mouse EST Project
            Washington University School of Medicine
            4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: mouseest@watson.wustl.edu
            This clone is available royalty-free through LLNL ; contact the
            IMAGE Consortium (info@image.llnl.gov) for further information.
            MGI:956982
            Seq primer: -28m13 rev2 ET from Amersham
            High quality sequence stop: 389.
FEATURES             Location/Qualifiers
     source          1..399
                     /organism "Mus musculus"
                     /db_xref "taxon:10090"
                     /clone "IMAGE:1617682"
                     /clone_lib "Soares mouse hypothalamus NbHy"
                     /tissue_type "hypothalamus"
                     /lab_host "DH10B"
                     /note "Organ: brain; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st
                     strand cDNA was primed with a Not I - oligo(dT) primer [5'
                     TGTTACCAATCTGAAGTGGGAGCGGCCGCAAGTTTTTTTTTTTTTTTTTTTT
                     T 3']; double-stranded cDNA was ligated to Eco RI adaptors
                     (Pharmacia), digested with Not I and cloned into the Not I
                     and Eco RI sites of the modified pT7T3 vector. RNA
                     provided by Dr. Wolfgang Liedtke. Library went through
                     two rounds of normalization, and was constructed by Bento
                     Soares and M.Fatima Bonaldo."
BASE COUNT       78 a    117 c    122 g     82 t
ORIGIN

  Query Match              7.6%;  Score 18;  DB 14;  Length 399;
  Best Local Similarity   100.0%;  Pred. No. 69;
  Matches   18;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy     50 tggctcaggctccctcag 67
          ||||||||||||||||||
Db    237 TGGCTCAGGCTCCCTCAG 254


RESULT 24
AW997626
LOCUS       AW997626     420 bp    mRNA            EST       [illegible]
DEFINITION  RC6-BN0052-170200-011-E10 BN0052 Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW997626
VERSION     AW997626.1  GI:8257860
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 420)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
            ,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55 11 2704922
            Fax: +55 11 2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=RC6-BN0052-170
            200-011-E10&t3=2000-02-17&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 28
            High quality sequence stop: 419.
FEATURES             Location/Qualifiers
     source          1..420
                     /organism "Homo sapiens"
                     /db_xref "taxon:9606"
```

/clone_lib="BN0052"
/dev_stage="Adult"
/note="Organ: breast_normal; Vector: pucl8; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
BASE COUNT 131 a 72 c 91 g 124 t 2 others
ORIGIN

Query Match 7.6%; Score 18; DB 123; Length 420;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 42 cctatttttgactcaggc 59
||||||||||||||||||
Db 162 CGTGTTTTTGGCTCAGGC 179

RESULT 25
BF320551/c
LOCUS BF320551 439 bp mRNA EST 29-DEC-2000
DEFINITION uz54d06.x1 NCI_CGAP_Mam6 Mus musculus cDNA clone IMAGE:3672875 3', mRNA sequence.
ACCESSION BF320551
VERSION BF320551.1 GI:11269526
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 439)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Jeffrey Green M.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
image.llnl.gov/image/html/iresources.shtml

MGI:1433643
High quality sequence stop: 416.
FEATURES Location/Qualifiers
source 1..439
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone="IMAGE:3672875"
/clone_lib="NCI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: SalI; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigator providing samples: Jeffrey Green, M.D., NIH"
BASE COUNT 147 a 95 c 70 g 127 t
ORIGIN

Query Match 7.6%; Score 18; DB 147; Length 439;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 199 tatttgtttctgtagaaa 216
||||||||||||||||||
Db 424 TCTTTCTTTCTCTACAAA 407

Search completed: October 9, 2001, 15:16:14
Job time: 4054 sec